

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: January 11, 2003, 15:49:42 ; Search time 4589 Seconds

(without alignments)
16913.747 Million cell updates/sec

Title: US-09-810-796-3

Sequence: 1 atgaagagatgtgagctcggg.....ctcatgtcaactgaatcaa 2667

Scoring table: IDENTITY_NUC
Gapex 10.0, Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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- 41: em_htg_other:*

Pred. No. is the number of results predicted by chance to have a

Score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	2662.2	99.8	2772	6	AX268474 Sequence
2	2662.2	99.8	3111	6	AX268476 Sequence
3	2630	98.6	2694	6	AX322509 Sequence
4	2625.2	98.4	3137	6	AX056817 Sequence
5	2625.2	98.4	3137	6	AF202977 Homo sapi
6	2617.2	98.1	3074	6	AX253254 Sequence
7	2617.2	98.1	3074	6	AX253254 Sequence
8	2617.2	98.1	3074	6	AF249278 Homo sapi
9	2507.6	94.0	2832	9	AF263835 Homo sapi
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11	963.4	36.1	1691	9	HSAG272519 Human DNA
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14	753.4	28.2	179192	2	AC095904 Rattus no
15	492	18.4	2335	6	AX032994 Sequence
16	492	18.4	2335	6	AX456863 Sequence
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ALIGNMENTS

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LOCUS	AX268474				
DEFINITION	Sequence 1 from Patent WO0175108.				
ACCESSION	AX268474				
VERSION	AX268474.1	GI:16541652			
KEYWORDS					
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
TITLE	Hu, Y., Kieck, J. A., Turner, A. C., Nehls, M. C., Friedrich, G. B., Zambrowicz, B. and Sands, A. T.				
	Human ion channel protein and polynucleotides encoding the same				

JOURNAL Patent: WO 0175108-A 1 11-OCT-2001;
 Lexicon Genetics Incorporated (US)
 Location/Qualifiers
 FEATURES
 source /organism="Homo sapiens"
 /db_xref="taxon:9606"
 ORIGIN
 BASE COUNT 715 a 700 c 713 g 644 t

Query Match 99.8%; Score 2662.2; DB 6; Length 2772;
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 Matches 2664; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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 1801 CAGATCCCAACCTTTTGAATGTGAACAGATCTGACTATCAAAAGCCTGTGGATAGCAAA 1860
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 2026 TCGAGAGGCTCGAGTTCATTTGAGCGCAATGAGTTCAAGTCCGAGACTTTTTCAGCGG 2085
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Db	2146	GCAGTGGACGCCACCAACACCATTTGCAACCAATAATACGGGACCCCAAGCCAGCAGCC	2205
Oy	2101	CCAAACAATTTACAGATGACACCTCTCTCCAGCCATCAAGCATCTGCCCAGCCAGAA	2160
Db	2206	CCAAACAATTTACAGATGACACCTCTCTCCAGCCATCAAGCATCTGCCCAGCCAGAA	2265
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Db	2326	GTTGCTCCAGAAATTTGATGATTTGCAAGTCAATATCTGACCAAGACCTGTTATG	2385
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Db	2446	GACTTGGGCAATCTTTGCTGTCGAAAACTGATAGTTCGACCGAGAACTGATAT	2505
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Oy	2521	ACTTTGATGCGGACCGACCGCTGCGGAGGAGCTGCTTTGCACTGACACTCTTAAG	2580
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Oy	2581	ACTGGAAGTGCAGATCTCTGAGAGCATTTGTAAGGAGAGAAATACAGATGCTT	2640
Db	2686	ACTGGAAGTGCAGATCTCTGAGAGCATTTGTAAGGAGAGAAATACAGATGCTT	2745
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Db	2746	AGCTTGCTCATGTCACAACTGAATTA	2772
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DEFINITION	Sequence 3 from Patent W00175108.		linear PAT 29-OCT-2001
ACCESSION	AX268476		
VERSION	AX268476.1	GI:16541653	
KEYWORDS	human.		
SOURCE	human.		
ORGANISM	human sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
AUTHORS	Hu, Y., Kieke, J.A., Turner, A.C., Nehls, M.C., Friedrich, G.B., Zambrowicz, B. and Sands, A.T.		
JOURNAL	Human Ion channel protein and polynucleotides encoding the same Patent: WO 0175108-A 3 11-OCT-2001.		
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Oy	121	AGGAGAGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG	180
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[illegible]

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QY	2521	ACGTTTGATGCCGACCGACCGACCGCTGCCAGGGAAGCTGCTTTGCATCAACCTCTAAG	2580
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LOCUS	AX322509	2694 bp	linear
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ACCESSION	AX322509		
VERSION	AX322509.1	GI:18093555	
KEYWORDS			
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	1 Dowerzky,S.I., Ramanathan,C.S., Trojnecki,J.T., Boissard,C.G. and Gribkoff,V.K.		
TITLE	Human kcnq5 potassium channel, methods and compositions thereof		
JOURNAL	Patent: WO 0192526-A 1 06-DEC-2001.		
FEATURES	Bristol-Myers Squibb Company (US)		
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Db	61	GACGGCTGTACTGCTGGGCGACCGCGCGCGCAAGCTTGTGGCGGCGCGTGGCCTG	120


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ACCESSION AF202977
VERSION AF202977.1 GI:7798695
KEYWORDS
SOURCE Homo sapiens.
ORGANISM Homo sapiens.
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AUTHORS Schroeder,B.C., Hechenberger,M., Weinreich,F., Kubisch,C. and Jentsch,T.J.
TITLE KCNO5, a novel potassium channel broadly expressed in brain, mediates M-type currents
JOURNAL J. Biol. Chem. 275 (31), 24089-24095 (2000)
MEDLINE 20379054
PUBMED 10816568
REFERENCE 2 (bases 1 to 3137)
AUTHORS Schroeder,B.C., Hechenberger,M., Weinreich,F., Kubisch,C. and Jentsch,T.J.
TITLE Direct Submission
JOURNAL Submitted (09-NOV-1999) ZMNH, Hamburg University, Martinistrasse 85, Hamburg 20246, Germany
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 VERSION AX253254.1 GI:16073802
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 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 3074)
 AUTHORS Lerche, C., Scherer, C., Seeböhm, G., Busch, A. and Steimeyer, K.
 TITLE Potassium channel protein kno5, a target for diseases of central
 JOURNAL nervous system and cardiovascular system
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 LOCUS AF263835 2832 bp mRNA linear PRI 01-JUN-2000

Query Match 80.8%; Score 2155; DB 10; Length 3108;
Best Local Similarly 89.0%; Pred. No. 0; Mismatches 263; Indels 27; Gaps 1;
Matches 2348; Conservative 0;

ORIGIN
Query Match 80.8%; Score 2155; DB 10; Length 3108;
Best Local Similarly 89.0%; Pred. No. 0; Mismatches 263; Indels 27; Gaps 1;
Matches 2348; Conservative 0;
1 GGGGAGGAGGCTGCTACTGCTGGGACCCGCGCGCCAGCTTGTTGGCGCGCGGTG 116
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237 CCTGTACACGAGCTGGAGAGACCCCGCGGCTGGGCGTTCACTACCGCTTCTTTT 296
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181 TCTGTACACAGCTGGAGAGCAGCCCGCGGCTGGGCGTTCTACACAGCGGCTTCTTT 240
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357 ATTGCCCTCAAGTGGCTCTGATCTGAGTTGAGTTGATGATGCTGCTTGTGTTGA 416
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537 ACCAGTGTGTTCTGCAAAAACCTGAGGTAATATTTTGGCCAGCTGCACTGAGAGCT 596
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717 TTTGTTCTTATTTTTCGTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 776
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777 GTTTTCTACATGAGATGCTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 836
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721 GTTTTCTACATGAGATGCTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 780
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837 TGGAGACAAACTCCCTAATGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 896
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781 CGAGAGCAAAACCTCCCTAATGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 840
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1141 CATTAGAGAGAGCAAGCATCAGTGTGACAGAGATGATGATGATGATGATGATGATGAT 1200
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2070 CCAAAATTAATGAGGAGCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2129
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2041 CCAAAATTAATGAGGAGCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2100
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JOURNAL
REFERENCE
AUTHORS

unpublished
2 (bases 1 to 162123)

TITLE
JOURNAL
REFERENCE
AUTHORS

Submitted
Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 162123)

TITLE
JOURNAL
COMMENT

Submitted
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Jun 21, 2002 this sequence version replaced g1:21431285.
All repeats were identified using RepeatMasker:
Smith, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html

Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence.submissions@genome.wi.mit.edu
Project Information
Center project name: L24884
Center clone name: 496_H_1
Sequencing vector: Plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 159326 bases at least Q40
Consensus quality: 160353 bases at least Q30
Consensus quality: 160941 bases at least Q20
Insert size: 160000; agarose-1p

Insert size: 161323; sum-of-contigs
Quality coverage: 8.7 in Q20 bases; agarose-1p
Quality coverage: 8.6 in Q20 bases; sum-of-contigs

NOTE: This is a 'working draft' sequence. It currently
consists of 9 contigs. Gaps between the contigs
are represented as runs of N. The order of the pieces
is believed to be correct as given, however the sizes
of the gaps between them are based on estimates that have
been provided by the submitter.
This sequence will be replaced
by the finished sequence as soon as it is available and
the accession number will be preserved.

1
617: contig of 617 bp in length
618 717: gap of 100 bp
718 2736: contig of 2019 bp in length
2737 2836: gap of 100 bp
2837 5807: contig of 2971 bp in length
5808 5907: gap of 100 bp
5908 19603: contig of 13696 bp in length
19604 19703: gap of 100 bp
19704 34958: contig of 15255 bp in length
34959 35058: gap of 100 bp
35059 52976: contig of 17918 bp in length
52977 53076: gap of 100 bp
53077 84088: contig of 31012 bp in length
84089 84188: gap of 100 bp
84189 121320: contig of 37032 bp in length
121321 121320: gap of 100 bp
121321 162123: contig of 40803 bp in length.

FEATURES
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Query Match 28.8%; Score 767.6; DB 2; Length 162123;
Best Local Similarity 87.2%; Pred. No. 4.9e-186;
Matches 842; Conservative 0; Mismatches 124; Indels 0; Gaps 0;

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Db 136323 CAGGTCCAGTCCATGAGCTCCAGGTGACGACGCTTCTAGTACATGATCAACAGGCTCT 136264
QY 1762 CGGAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1821
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QY 1822 GAGACAGATCTGACTATCAAGCCCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1881
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QY 2122 CCTCTCTCCACCATCAAGCATCTGCCAGCCAGAACTCTGCACCTTAACCCCTCA 2181
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QY 2182 GGGTTCAGGAAGCATTTTGTGACGTCAACCGCTGCTGTGCTCCAGGAATGTT 2241
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QY 2361 TGGCAAAACCTATCATGAGTGCACCGCAAGTGAATATACACTTTCAGGAGTGAAT 2420
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QY 2541 GCTTCGAGAGAGTGGTCCGAGAGACAGACACTTTTATGCCGAGTGAAGTGAAGTGAATC 2600
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QY 2601 TCAGAGCATTTTGAAGAGAGAGAGATGACATGACCTTGCCTGATGTCATGTCAACT 2660
Db 176468 TCAGAGCATTTTGAAGAGAGAGAGATGACATGACCTTGCCTGATGTCATGTCAACT 176409
QY 2661 GAAATTA 2667
Db 176408 GAACTTA 176402

RESULT 15
AX032994 2335 bp DNA linear PAT 21-SEP-2000
LOCUS AX032994 2335 bp DNA linear PAT 21-SEP-2000
DEFINITION Sequence 1 from Patent WO0044786.
ACCESSION AX032994
VERSION AX032994.1 GI:10279897
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
Jentsch,T.J.
TITLE Novel potassium channels and genes encoding these potassium
channels
JOURNAL Patent: WO 0044786-A 1 03-AUG-2000;
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FEATURES
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BASE COUNT 396 a 812 c 719 g 408 t
ORIGIN
Query Match 18.4%; Score 492; DB 6; Length 2335;
Best Local Similarity 59.3%; Pred. No. 2,2e-115;
Matches 1087; Conservative 0; Mismatches 555; Indels 192; Gaps 7;
QY 217 TACCGGGGGGTGCAAGCACTACCTGCAAGTGTGAGAGACCCGGCGCTGGCGCTTC 276
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Db 500 ATCTGCTTGTGCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 559
QY 457 TATAGAGATGCAAGAGAGTGTGCTGCAAGAGCTTCTGCTGCTGCTGCTGCTGCTGCT 516
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QY 577 AGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 636
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QY 637 AGGAGAGCAGCTTGAAGATTAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 696
Db 740 CCGGAGAGCAGCTTGAAGATTAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 799
QY 697 ACAGCTGTGATAGAGATTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 756
Db 800 ACCGCTGTGATAGAGATTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 859
QY 757 GAAAGGATGCAATTAAGATTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 816
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Db 1922 AGCATGATGGGACGCGGTGTCAAGGTGGAGAACAGGTGCAATCAGACACAGCTG 1981
QY 1729 GACTGCCCTACTAGACATCTATCAACAGGTCTTGGAAAAGGCTGCTGCTGCTGCT 1788
Db 1982 GACCTGTGTTGGGTCTTATTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2035
QY 1789 TTGCTTATTCAGATCCACCTTTTGAATGTGAACAGACATCTGACTATCAAAAGCCT 1848
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QY 1849 GTGATAGAAAGATCTTTCGGGTTCCGACAAA 1882
Db 2096 GTGGACACGAGGACATCTCCGCTCCGACAGA 2129

Search completed: January 11, 2003, 17:21:14
Job time : 4901 secs

XX Jiegla TJ;
XX WPI: 2001-611467/70.
XX P-PSDB: AAU09021.
XX
XX Polyptides and polynucleotides of potassium channel KCNQ5 for
XX identifying a compound modulating ion flux in eukaryotic cell or cell
XX membrane expressing the protein, comprises KCNQ alpha
XX subunits
XX
XX Claim 5: Page 63-64; 78pp; English.
XX
XX The invention relates to an isolated polypeptide comprising an
XX alpha-subunit of a KCNQ potassium channel, with a subsequence having
XX 638 sequence identity to amino acids 343-640 of hKCNQ5-1 amino acid
XX sequence and forms a KCNQ potassium channel having the characteristic of
XX voltage-gating with at least an additional KCNQ alpha-subunit. Also
XX included in the scope of the invention are the nucleic acids encoding
XX hKCNQ5 (including splice variants encoding hKCNQ5-1 and hKCNQ5-2),
XX expression vectors encoding them, antibodies against them, the use of
XX 3-dimensional computer modelling to identify molecules that bind to a
XX KCNQ containing potassium channel and modulate ion flux through the
XX channel. The KCNQ polypeptide is useful for identifying a compound that
XX increases or decreases ion flux through a potassium channel expressed in
XX an eukaryotic host cell or cell membrane. The compound (and the
XX KCNQ nucleic acid when used in gene therapy) is useful as
XX a pharmaceutical agent for treating diseases involving abnormal ion flux,
XX such as disorders of the central nervous system, such as epilepsy,
XX migraines, hearing and vision problems, psychotic disorders, seizures,
XX learning and memory disorders, stroke and pain. The antibodies are
XX useful for detecting a KCNQ5 polypeptide in a human tissue and the
XX use of a nucleotide sequence of KCNQ5 to search computer databases to
XX find variants of the sequence which are associated with disease states,
XX is useful for screening mutations of KCNQ5. The present sequence is
XX a splice variant of hKCNQ5 encoding hKCNQ5-2.
XX
SQ Sequence 2667 BP; 701 A; 667 C; 660 G; 639 T; 0 other;
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 2667; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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121 AGGAGAGCGCGCGGCGGCAAGCGAGGGGCGCGGATGAGCTGTGGGAGACCGCTCT 180
181 TACACGAGTAGGACAGAGCTGCGCGGCAAGCTCAAGTACCGGCGGTCAGAACTACTG 240
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421 ATCATTCGATCTGCTGCGGGTGTGCTGTTTCGATATAGAGATGCGAAGAGACTG 480

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QY 541 GTTGTTCGCAAAACCTCAGGGAATATATTTTCCACGCTGTCAGTCAAGTCTCCGT 600
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QY 661 GGTTCAGTGGTTATGTCACACAGAGAAATTAATCACAGTGGTATAGATTTTGG 720
Db 661 GGTTCAGTGGTTATGTCACACAGAGAAATTAATCACAGTGGTATAGATTTTGG 720
QY 721 GTTCTATTTTTCGTTCTCTTCTGCTATCTGTGTAAGAAAGATGCAATTAAGAGTTT 780
Db 721 GTTCTATTTTTCGTTCTCTTCTGCTATCTGTGTAAGAAAGATGCAATTAAGAGTTT 780
QY 781 TCTACATATGCAATGCTCTCTGCTGGGCGCAATTAATGACACTATTTGGCTATGGA 840
Db 781 TCTACATATGCAATGCTCTCTGCTGGGCGCAATTAATGACACTATTTGGCTATGGA 840
QY 841 GACAAACCTCCCTAATCTTGGCTGGGAAGATTTGCTTCTGCAAGGCTTTCACCTCTGGC 900
Db 841 GACAAACCTCCCTAATCTTGGCTGGGAAGATTTGCTTCTGCAAGGCTTTCACCTCTGGC 900
QY 901 ATTTCTTTCTTTGACATCTCTCTGCGGCAATTTGAGTGGCTGAGTTTTCATTAAGTACAA 960
Db 901 ATTTCTTTCTTTGACATCTCTCTGCGGCAATTTGAGTGGCTGAGTTTTCATTAAGTACAA 960
QY 961 GAACACACCGCGGCAAGAACTTTGAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 1020
Db 961 GAACACACCGCGGCAAGAACTTTGAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 1020
QY 1021 TGTGTTGGGCTAGTTCGCGAGTGTGAGAAATCTGTTTCATTTGCAATCTGAAAGCA 1080
Db 1021 TGTGTTGGGCTAGTTCGCGAGTGTGAGAAATCTGTTTCATTTGCAATCTGAAAGCA 1080
QY 1081 CACTTGAAGCCCTTGACACCTGACGCTTACCAATCAGAACTAAGTTTAAAGAGCA 1140
Db 1081 CACTTGAAGCCCTTGACACCTGACGCTTACCAATCAGAACTAAGTTTAAAGAGCA 1140
QY 1141 GTGCGCATGGCTAGCCCGAGGCGGCAAGTATTAAGACCGCAAGCCGCAATGATGAG 1200
Db 1141 GTGCGCATGGCTAGCCCGAGGCGGCAAGTATTAAGACCGCAAGCCGCAATGATGAG 1200
QY 1201 AGGAGGTCCCAAGACGACATCATCAGGCGGCAAGTATTAAGACCGCAAGCCGCAATGAG 1260
Db 1201 AGGAGGTCCCAAGACGACATCATCAGGCGGCAAGTATTAAGACCGCAAGCCGCAATGAG 1260
QY 1261 TGGAGCTTCAACGACGCAAGCCGCTTCCGCGCTGCTGCGCTTCAAAAGTTCTAGCCA 1320
Db 1261 TGGAGCTTCAACGACGCAAGCCGCTTCCGCGCTGCTGCGCTTCAAAAGTTCTAGCCA 1320
QY 1321 AAACCACTGATGATGTCGACACAGCCCTTGGCACTGATGATGATGATGATGATGATGATG 1380
Db 1321 AAACCACTGATGATGTCGACACAGCCCTTGGCACTGATGATGATGATGATGATGATGATG 1380
QY 1381 TGGCAGTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1440
Db 1381 TGGCAGTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1440
QY 1441 ATCAGAAATTAATGAAATTTGATGTTGCAAAAGAAAGTTTAAAGAAAGTTTAAAGAAAGTT 1500
Db 1441 ATCAGAAATTAATGAAATTTGATGTTGCAAAAGAAAGTTTAAAGAAAGTTTAAAGAAAGTT 1500
QY 1501 GATGTAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1560
Db 1501 GATGTAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1560

OY 1561 AAAAGCCTTCAAAACACGTGTGATCAAAATCTTGAAAAAGGCGCAAAATCACATCAGATAG 1620
|||||
DB 1561 AAAAGCCTTCAAAACACGTGTGATCAAAATCTTGAAAAAGGCGCAAAATCACATCAGATAG 1620
OY 1621 AAGAGCCGAGAGAAAATTAACAGCAGACATGAGACCAACAGATCTCATGATGCTGGGT 1680
|||||
DB 1621 AAGAGCCGAGAGAAAATTAACAGCAGACATGAGACCAACAGATCTCATGATGCTGGGT 1680
OY 1681 CGGGTGTCAAGGTGTAAGAAAACAGGTACAGTCCATAGAGTCCAAAGCTGGAGCTGCTACTA 1740
|||||
DB 1681 CGGGTGTCAAGGTGTAAGAAAACAGGTACAGTCCATAGAGTCCAAAGCTGGAGCTGCTACTA 1740
OY 1741 GACATCTATCAACAGGTCCTTCGAAAAGGCTCTGCTCAGCCCTCGGTTGGCTTCATATTC 1800
|||||
DB 1741 GACATCTATCAACAGGTCCTTCGAAAAGGCTCTGCTCAGCCCTCGGTTGGCTTCATATTC 1800
OY 1801 CAGATCTCCACCTTTTAATGATGAACAGACATCTGACTATCAAAAGCCCTGTGGATAGCAA 1860
|||||
DB 1801 CAGATCTCCACCTTTTAATGATGAACAGACATCTGACTATCAAAAGCCCTGTGGATAGCAA 1860
OY 1861 GATCTTTCGGGTCCGCAAAACAGTGGCTGTATCCAGATCACTAGTCCAAACATC 1920
|||||
DB 1861 GATCTTTCGGGTCCGCAAAACAGTGGCTGTATCCAGATCACTAGTCCAAACATC 1920
OY 1921 TCGAGAGGCTGCGAGTTCAATCTGACGCCCAATGAGTTCAGTGGCCAGACTTTCAGCG 1980
|||||
DB 1921 TCGAGAGGCTGCGAGTTCAATCTGACGCCCAATGAGTTCAGTGGCCAGACTTTCAGCG 1980
OY 1981 CTTAGCCCTACTATGACACATGCAAGCAACAGAGTGGCAATTAAGTCAAAAGGATGGCTCA 2040
|||||
DB 1981 CTTAGCCCTACTATGACACATGCAAGCAACAGAGTGGCAATTAAGTCAAAAGGATGGCTCA 2040
OY 2041 GGAGTGGGAGCCACCAACCATTTGCAAAACCAATAATACCGCACCAGCCAGCCAGCACCC 2100
|||||
DB 2041 GGAGTGGGAGCCACCAACCATTTGCAAAACCAATAATACCGCACCAGCCAGCCAGCACCC 2100
OY 2101 CCAACAACCTTTAGATGCCACCTCTCTCCAGCCATCAAGCATCTGCCCAGAGCCAGAA 2160
|||||
DB 2101 CCAACAACCTTTAGATGCCACCTCTCTCTCCAGCCATCAAGCATCTGCCCAGAGCCAGAA 2160
OY 2161 ACTCTGACCCCTTAACCTGCGACGCTTACAGAAACATTTCTGACGTCACCACTGCTT 2220
|||||
DB 2161 ACTCTGACCCCTTAACCTGCGACGCTTACAGAAACATTTCTGACGTCACCACTGCTT 2220
OY 2221 GTTGCTCCAGAAAATGTTCAGGTTGCACAGTCAATCTCACCAAGGACCGTTCTATG 2280
|||||
DB 2221 GTTGCTCCAGAAAATGTTCAGGTTGCACAGTCAATCTCACCAAGGACCGTTCTATG 2280
OY 2281 AGGAAAAGCTTTGACATGGGAGAGAAACTCTGTGCTGTCTGTCATGTCGCGCAAG 2340
|||||
DB 2281 AGGAAAAGCTTTGACATGGGAGAGAAACTCTGTGCTGTCTGTCATGTCGCGCAAG 2340
OY 2341 GACTTGGGCAAAATCTTTGTCTGTGCAAAACCTGATCAGGTGCGAGCACTGATATA 2400
|||||
DB 2341 GACTTGGGCAAAATCTTTGTCTGTGCAAAACCTGATCAGGTGCGAGCACTGATATA 2400
OY 2401 CAACTTTCAGGAGTGAAGTCAAGTGTCCAGAGGCGCAAGATTTTACCCCAAAATGG 2460
|||||
DB 2401 CAACTTTCAGGAGTGAAGTCAAGTGTCCAGAGGCGCAAGATTTTACCCCAAAATGG 2460
OY 2461 AGGGAATCCAAATTTGTTTATACATGATGAAGAGTGGTCCCGAAGAGACAGAAAGAC 2520
|||||
DB 2461 AGGGAATCCAAATTTGTTTATACATGATGAAGAGTGGTCCCGAAGAGACAGAAAGAC 2520
OY 2521 ACTTTTGAATCCGACCGCAGCCTGCCAGGGAAGCTCCCTTTGATCAGACTCTCTAAGG 2580
|||||
DB 2521 ACTTTTGAATCCGACCGCAGCCTGCCAGGGAAGCTCCCTTTGATCAGACTCTCTAAGG 2580
OY 2581 ACTGGAAGGTGCAGATCATCTCAGACACTTTGTAAGGAGAGAAATACAGATGCTCC 2640
|||||
DB 2581 ACTGGAAGGTGCAGATCATCTCAGACACTTTGTAAGGAGAGAAATACAGATGCTCC 2640

OY 2641 AGCTTGCTCATGTCAAACTGAATAA 2667
|||||
DB 2641 AGCTTGCTCATGTCAAACTGAATAA 2667
RESULT 2
AAH43633
ID AAH43633 standard; cDNA; 2772 BP.
XX
AC AAH43633;
XX
DT 21-JAN-2002 (first entry)
XX
DE Human ion-channel forming protein ORF.
XX
KW Ion-channel forming protein; voltage-gated potassium channel;
XX fetal; brain; thymus; prostate; heart; skeletal muscle; probe; ss.
OS Homo sapiens.
XX
PN W0200175108-A1.
XX
PD 11-OCT-2001.
XX
PF 03-APR-2001; 2001WO-US10875.
XX
PR 03-APR-2000; 2000US-194255P.
XX
PA (LEXI-) LEXICON GENETICS INC.
XX
PI Hu Y, Kiehe JA, Turner AC, Nehls MC, Friedrich G, Zambrowicz B;
PI Sands AT;
XX
DR WPI: 2001-656987/75.
XX
P-PSDB: AAB47678.
PT New human ion channel protein and polynucleotides encoding the protein,
PT useful in diagnosing or treating diseases, in drug screening, and in
PT clinical trial monitoring
XX
PS Claim 1: Page 34-35; 41pp; English.
XX
P5 The sequences in AAH43633-34 encode a novel ion-channel forming protein.
CC The protein shares structural similarity with mammalian ion channel
CC proteins, particularly voltage-gated potassium channel proteins. The
CC protein is expressed in many human cell lines including fetal brain,
CC brain, thymus, prostate, heart and skeletal muscle. The novel protein
CC can be used in the diagnosis or treatment of diseases, in drug
CC screening, and in clinical trial monitoring. The oligonucleotides may
CC be used as hybridization probes for screening libraries, and assessing
CC gene expression patterns (particularly using a micro array or high
CC throughput chip format). The nucleic acids and novel protein can also be
CC used in the identification, selection and validation of novel molecular
CC targets for drug discovery, to screen collections of genetic material
CC from patients who have a particular medical condition, to identify
CC mutations associated with a particular disease, as a diagnostic or
CC prognostic assay, and to screen for drugs which can be used to treat
CC symptomatic or phenotypic manifestations of perturbing the normal
CC function of novel human protein. The polypeptides are further used in
CC generating antibodies.
XX
SQ Sequence 2772 BP; 715 A; 700 C; 713 G; 644 T; 0 other;
Query Match 99.8%; Score 2662.2; DB 22; Length 2772;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2664; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY 1 ATGAAGGATGTGAGTCCGGGCGGAGGCTGTGTAACTCGGCAGCGCCAGGGGC 60
|||||
DB 106 ATGAAGGATGTGAGTCCGGGCGGAGGCTGTGTAACTCGGCAGCGCCAGGGGC 165
|||||
OY 61 GACGGCTTCTACTGCTGGGCAACCCGCGCGCACCTTGTTGGCGCGCGGTGGCTTG 120
|||||

Db 166 GACGCGCTGCTACTGCTGGGACACCCGCGCGCCACGCTCGTGGCGGCGGCTGGGCTG 225
Qy 121 AGGAGAGAGCGCGCGGGAAGAGAGGGGCGCGGATGAGCCTGCTGGGGAAGCCGCTCTCT 180
Db 226 AGGAGAGAGCGCGCGGGAAGAGAGGGGCGCGGATGAGCCTGCTGGGGAAGCCGCTCTCT 285
Qy 181 TACACGAGTAGCCAGAGAGCTGGCGGCGCAACGTCAAGTACCGGCGGGTGCAGAACTACTG 240
Db 286 TACACGAGTAGCCAGAGAGCTGGCGGCGCAACGTCAAGTACCGGCGGGTGCAGAACTACTG 345
Qy 241 TACACAGTGTGAGAGAGACCCGCGGCGTGGCGCTTCATCTACCAGCTTTCTTTTCTC 300
Db 346 TACACAGTGTGAGAGAGACCCGCGGCGTGGCGCTTCATCTACCAGCTTTCTTTTCTC 405
Qy 301 CTGTGCTTTGGTGGTGTGATTTTGTGAGTGTTCAGATCCCTGAGCAGCAAAATG 360
Db 406 CTGTGCTTTGGTGGTGTGATTTTGTGAGTGTTCAGATCCCTGAGCAGCAAAATG 465
Qy 361 GCGTCAAGTTGCGCTTGTGATCTGAGTTCGTGANGATTCGCTCTTTGGTTGAGTTC 420
Db 466 GCGTCAAGTTGCGCTTGTGATCTGAGTTCGTGANGATTCGCTCTTTGGTTGAGTTC 525
Qy 421 ATCTTGAATCTGCTGCTCGGCGTGTCTGTTCATATAGAGATGGCAGAGAGACTG 480
Db 526 ATCTTGAATCTGCTGCTCGGCGTGTCTGTTCATATAGAGATGGCAGAGAGACTG 585
Qy 481 AGGTTGCTGCAAAAGCCCTCTGCTGATAGATACATGTTCTTATGCTTCAATAGCA 540
Db 586 AGGTTGCTGCAAAAGCCCTCTGCTGATAGATACATGTTCTTATGCTTCAATAGCA 645
Qy 541 GTTGTCTTCTGCAAAAACTCAGGGTAAATATTTTTCACAGCTTCGACTCAGAACTCTCGT 600
Db 646 GTTGTCTTCTGCAAAAACTCAGGGTAAATATTTTTCACAGCTTCGACTCAGAACTCTCGT 705
Qy 601 TTCTTACAGATCTCCGATGCTGGCGATGACCGAAGGGAGGACCTTGGAAATTTCTG 660
Db 706 TTCTTACAGATCTCCGATGCTGGCGATGACCGAAGGGAGGACCTTGGAAATTTCTG 765
Qy 661 GGTTCAAGTGTATGCTCAGACAGCAAGAAATTAATCAGAGCTGTGATAGAGATTTTG 720
Db 766 GGTTCAAGTGTATGCTCAGACAGCAAGAAATTAATCAGAGCTGTGATAGAGATTTTG 825
Qy 721 GTTCTATATTTTTCGCTCTTCTCTGTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
Db 826 GTTCTATATTTTTCGCTCTTCTCTGTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 885
Qy 781 TCTCATATGAGATGCTCTCTGGTGGGCAATTTACATTTGCACTATTTGGCTATGGA 840
Db 886 TCTCATATGAGATGCTCTCTGGTGGGCAATTTACATTTGCACTATTTGGCTATGGA 945
Qy 841 GACAAACTCCCTTAACCTTGGCTGGGAAGATGCTTTCAGAGCTTTGACTCCCTGGC 900
Db 946 GACAAACTCCCTTAACCTTGGCTGGGAAGATGCTTTCAGAGCTTTGACTCCCTGGC 1005
Qy 901 ATTTCCTTCTTTCGACTTCGCGCGGATTCCTGCTCAGGTTTTCATTTAAAGTACAA 960
Db 1006 ATTTCCTTCTTTCGACTTCGCGCGGATTCCTGCTCAGGTTTTCATTTAAAGTACAA 1065
Qy 961 GAACAACAGCGCCAGAAACACTTTGAGAAAAGAGAACCCAGCTGCCAATCTCATTCAG 1020
Db 1066 GAACAACAGCGCCAGAAACACTTTGAGAAAAGAGAACCCAGCTGCCAATCTCATTCAG 1125
Qy 1021 TGTGTTTGGCTAGTATGAGAGCTGATGAAATCTGTTCCATTTGCAACTGGAAGCCA 1080
Db 1126 TGTGTTTGGCTAGTATGAGAGCTGATGAAATCTGTTCCATTTGCAACTGGAAGCCA 1185
Qy 1081 CACTTGAAGGCTTGCACACCTGCAGCCCTTACCAATCAGAAAGCTTAAGTTTAAAGAGCGA 1140
Db 1186 CACTTGAAGGCTTGCACACCTGCAGCCCTTACCAATCAGAAAGCTTAAGTTTAAAGAGCGA 1245
Qy 1141 GTGGGCAATGGCTAGCCCAAGGGGCGCAGAGTATTTAGAGCCGACAGCCTCAGTAGTGAC 1200
Db 1246 GTGGGCAATGGCTAGCCCAAGGGGCGCAGAGTATTTAGAGCCGACAGCCTCAGTAGTGAC 1305

Qy 1201 AGGAGTCCCAAGCACCGCATCAGAGCGAGGCGAGTCCACCAAAAGTCAGAAAGAC 1260
Db 1306 AGGAGTCCCAAGCACCGCATCAGAGCGAGGCGAGTCCACCAAAAGTCAGAAAGAC 1365
Qy 1261 TGGAGCTTCAAGCAGCCGAACCCGCTTCCGGCCCTCGCTGGCGCTCAAAAGTTCAGCCA 1320
Db 1366 TGGAGCTTCAAGCAGCCGAACCCGCTTCCGGCCCTCGCTGGCGCTCAAAAGTTCAGCCA 1425
Qy 1321 AAACCAATATAGATCTGACACAGCCCTTGGCAGCTATGATATATGATGAAAAAGGA 1380
Db 1426 AAACCAATATAGATCTGACACAGCCCTTGGCAGCTATGATATATGATGAAAAAGGA 1485
Qy 1381 TGGCAGTGTGATGATCAGTGAAGACCTCAGCCACCACTTAAACCTGATTCAGACT 1440
Db 1486 TGGCAGTGTGATGATCAGTGAAGACCTCAGCCACCACTTAAACCTGATTCAGACT 1545
Qy 1441 ATCAGAAATATGAATTTCAATGTTGCAAAAGGAAGTTTAAAGAAAGTTACGTCCATAT 1500
Db 1546 ATCAGAAATATGAATTTCAATGTTGCAAAAGGAAGTTTAAAGAAAGTTACGTCCATAT 1605
Qy 1501 GATGTAAAGATGCTCATTTGACAAATATTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1560
Db 1606 GATGTAAAGATGCTCATTTGACAAATATTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1665
Qy 1561 AAAAGCCTTCAAAACAGCTGTGATCAAAATCTTGGAAAAGGCAATCAGATAG 1620
Db 1666 AAAAGCCTTCAAAACAGCTGTGATCAAAATCTTGGAAAAGGCAATCAGATAG 1725
Qy 1621 AAGAGCCGAGAGAAATTAACAGCAGAACATGAGACCAAGAGATCTCAGTAGTCTCGGT 1680
Db 1726 AAGAGCCGAGAGAAATTAACAGCAGAACATGAGACCAAGAGATCTCAGTAGTCTCGGT 1785
Qy 1681 GGGGTGCTAAGGTTGAAAAAGGTAACAGTACATGATAGTCAAGCTGAGTCTACTA 1740
Db 1786 GGGGTGCTAAGGTTGAAAAAGGTAACAGTACATGATAGTCAAGCTGAGTCTACTA 1845
Qy 1741 GACATCTATCAACAGGTCCTTCGAAAAGGCTCTGCTCAGCCCTCGCTTGGCTTCATTC 1800
Db 1846 GACATCTATCAACAGGTCCTTCGAAAAGGCTCTGCTCAGCCCTCGCTTGGCTTCATTC 1905
Qy 1801 CAGATCCACCTTTTGAATGTGAACAGACATCTGACTATCAAAAGCCCTGTGGATAGCAA 1860
Db 1906 CAGATCCACCTTTTGAATGTGAACAGACATCTGACTATCAAAAGCCCTGTGGATAGCAA 1965
Qy 1861 GATCTTGGGGTCCGACAAAACAGTGGCTGTATCCAGATCAAGTACAGGCAACATC 1920
Db 1966 GATCTTGGGGTCCGACAAAACAGTGGCTGTATCCAGATCAAGTACAGGCAACATC 2025
Qy 1921 TCGAGAGGCTGAGTTCATTTCTGAGCGCCAAATGAGTTCAAGTGGCCAGACTTTAGCGG 1980
Db 2026 TCGAGAGGCTGAGTTCATTTCTGAGCGCCAAATGAGTTCAAGTGGCCAGACTTTAGCGG 2085
Qy 1981 CTTAGCCCTACTATGCAAGTCAAGCAACACAGTGGCCAAATTAAGTCAAAAGCGATGCTCA 2040
Db 2086 CTTAGCCCTACTATGCAAGTCAAGCAACACAGTGGCCAAATTAAGTCAAAAGCGATGCTCA 2145
Qy 2041 GGAGTGGCAGCCCAACCAACCATTTGCAAAACCAATTAATACGGCAACCCAGCAAGCC 2100
Db 2146 GGAGTGGCAGCCCAACCAACCATTTGCAAAACCAATTAATACGGCAACCCAGCAAGCC 2205
Qy 2101 CCAACAACTTATCAGATATCCACCTCTCTCCAGCCATCAAGCAATCTGACCAGGCAAGAA 2160
Db 2206 CCAACAACTTATCAGATATCCACCTCTCTCTCCAGCCATCAAGCAATCTGACCAGGCAAGAA 2265
Qy 2161 ACTGTGACCCCTTAACCCCTGAGGCTTAACAGAAAGCAATTTCTGACGTACACCTGCTCT 2220
Db 2266 ACTGTGACCCCTTAACCCCTGAGGCTTAACAGAAAGCAATTTCTGACGTACACCTGCTCT 2325
Qy 2221 GTTGGCTCCAAAGAAATGTTCAGGTTTGCACAGTCAATCTCACCAAGGACCGTTCTATG 2280
Db 2326 GTTGGCTCCAAAGAAATGTTCAGGTTTGCACAGTCAATCTCACCAAGGACCGTTCTATG 2385

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Db 885 GTTCTATTATTTTCGCTTTCCTGCTCTATCTGTGAAAAAGATGCCAATTAAGAGTTT 944
OY 781 TCTACATATGAGATGCTCTCTGTGTGGGACAAATATACATTTGACACTATTTGGGTATGGA 840
Db 945 TCTACATATGAGATGCTCTCTGTGTGGGACAAATATACATTTGACACTATTTGGGTATGGA 1004
OY 841 GACAAATCTCCCTACTGCTGTGGGAGATTTGCTTTGCGAGCTTTTGCACCTCTTGGC 900
Db 1005 GACAAATCTCCCTACTGCTGTGGGAGATTTGCTTTGCGAGCTTTTGCACCTCTTGGC 1064
OY 901 ATTTCTTTTTCGACTCTGCTGCGGATTTTGTGCTGAGTTTTCATTAATAATACAA 960
Db 1065 ATTTCTTTTTCGACTCTGCTGCGGATTTTGTGCTGAGTTTTCATTAATAATACAA 1124
OY 961 GACAAACACCGCCAGAAACACTTTGAGAAAGAAAGAACCCAGCTGCCAACCCTATTCAG 1020
Db 1125 GACAAACACCGCCAGAAACACTTTGAGAAAGAAAGAACCCAGCTGCCAACCCTATTCAG 1184
OY 1021 TGTGTTGGGCTAGTTAGCAGCTGATGAGAAATCTGTTCCATTCGAACCTGGAGGCA 1080
Db 1185 TGTGTTGGGCTAGTTAGCAGCTGATGAGAAATCTGTTCCATTCGAACCTGGAGGCA 1140
OY 1081 CACTTGAAGGCTTGGACACCTGACAGCTTACCAATCAGAAAGCTAGTTTAAGAGGCA 1304
Db 1245 CACTTGAAGGCTTGGACACCTGACAGCTTACCAATCAGAAAGCTAGTTTAAGAGGCA 1200
OY 1141 GTGCGCATGGCTAGCCCGAGGGGCGAGAGTATTAAGAGCCGACAAAGCTCAGTAGTGAC 1260
Db 1305 GTGCGCATGGCTAGCCCGAGGGGCGAGAGTATTAAGAGCCGACAAAGCTCAGTAGTGAC 1364
OY 1201 AGGAGTCTCCCAAGACACGACATCAGACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1260
Db 1365 AGGAGTCTCCCAAGACACGACATCAGACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1320
OY 1261 TGGAGCTTCAAGAGCGAAGCCGCTTCGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCG 1484
Db 1425 TGGAGCTTCAAGAGCGAAGCCGCTTCGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCG 1380
OY 1321 AAACAGATGATGATGCTGACACAGCCCTTGGGAGCTGATGATGATGATGATGATGATG 1544
Db 1485 AAACAGATGATGATGCTGACACAGCCCTTGGGAGCTGATGATGATGATGATGATGATG 1440
OY 1381 TGGCAGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1604
Db 1545 TGGCAGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1500
OY 1441 ATCAGATTTATGAATTTATGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 1664
Db 1605 ATCAGATTTATGAATTTATGATTTGATTTGATTTGATTTGATTTGATTTGATTTGAT 1560
OY 1501 GATGTAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1724
Db 1665 GATGTAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1620
OY 1561 AAAAGCCTTCAACACGCTGTTGATCAATTTCTGAAAAAGGCAATCAGATCAATG 1784
Db 1725 AAAAGCCTTCAACACGCTGTTGATCAATTTCTGAAAAAGGCAATCAGATCAATG 1680
OY 1621 AAGAGCGAGAGAAATTAACAGACAGATGACACAGAGATGCTGATGCTGATGCT 1844
Db 1785 AAGAGCGAGAGAAATTAACAGACAGATGACACAGAGATGCTGATGCTGATGCTGAT 1740
OY 1681 CCGGTGCTCAAGGTGATGAAAAAGGTACAGTCAATGATCAATCAAGTGGAGCTGCT 1904
Db 1845 CCGGTGCTCAAGGTGATGAAAAAGGTACAGTCAATGATCAATCAAGTGGAGCTGCT 1800
OY 1741 GACATCTATCAACAGGCTCTTGGAAAGGCTCTGCTGAGCCCTGCTTGGCTTCAATTC 1964
Db 1905 GACATCTATCAACAGGCTCTTGGAAAGGCTCTGCTGAGCCCTGCTTGGCTTCAATTC 1860
OY 1801 CAGATCCCACTTTGAAATGAGACAGATCTGACTATCAAAAGCCCTGCTGATGAGCA 2024
Db 1965 CAGATCCCACTTTGAAATGAGACAGATCTGACTATCAAAAGCCCTGCTGATGAGCA

OY 1861 GATCTTTGGGTTTCCGACAAACAGGCGCTGATTCAGATATCACTAGTGGCAACATC 1920
Db 2025 GATCTTTGGGTTTCCGACAAACAGGCGCTGATTCAGATATCACTAGTGGCAACATC 2084
OY 1921 TCGAGAGGCTCCGAGTTCATCTGACGCAAAATGATGATGATGATGATGATGATGATG 2144
Db 2085 TCGAGAGGCTCCGAGTTCATCTGACGCAAAATGATGATGATGATGATGATGATGATG 2040
OY 1981 CTAGAGCTTACTATGACAGCTGACAGACAGAGGCTGCAATTAAGTCAAGGATGCTCA 2204
Db 2145 CTAGAGCTTACTATGACAGCTGACAGACAGAGGCTGCAATTAAGTCAAGGATGCTCA 2100
OY 2041 GCGATGCGACCCACCAACACCATTTGCAAAATTAATAGGCTACCAAGCCAGGAGCC 2264
Db 2205 GCGATGCGACCCACCAACACCATTTGCAAAATTAATAGGCTACCAAGCCAGGAGCC 2160
OY 2101 CCACACCTTTACAGATCCACCTCTCTCTCCAGGCTATCAAGATCTGCTCCAGGCGAGAA 2324
Db 2265 CCACACCTTTACAGATCCACCTCTCTCTCCAGGCTATCAAGATCTGCTCCAGGCGAGAA 2324
OY 2161 ACTCTGACCTTACACCTGACAGCTTACAGAAACATTTTGAAGTCCACACCTGCTT 2384
Db 2325 ACTCTGACCTTACACCTGACAGCTTACAGAAACATTTTGAAGTCCACACCTGCTT 2280
OY 2221 GTTGGCTCCAAAGAAATGTTGAGTTGACAGTCAATCTCACCAGAGCCGTTATG 2444
Db 2385 GTTGGCTCCAAAGAAATGTTGAGTTGACAGTCAATCTCACCAGAGCCGTTATG 2340
OY 2281 AGGAAAGGCTTTGACATGAGGAGGAGAAACCTGTTGCTGCTGCTGCTGCTGCTGCTG 2504
Db 2445 AGGAAAGGCTTTGACATGAGGAGGAGAAACCTGTTGCTGCTGCTGCTGCTGCTGCTG 2400
OY 2341 GACTTGGGCAATCTTTGCTGCTGCAAAACCTGATCAGGTCACGAGAACTGATTA 2564
Db 2505 GACTTGGGCAATCTTTGCTGCTGCAAAACCTGATCAGGTCACGAGAACTGATTA 2460
OY 2401 CAATCTTCAGGAGTGAAGTCAAGTGGCTCCAGAGGAGGAGGAGGAGGAGGAGGAGG 2624
Db 2565 CAATCTTCAGGAGTGAAGTCAAGTGGCTCCAGAGGAGGAGGAGGAGGAGGAGGAGG 2520
OY 2461 AGGGAATCCAAATGTTTATTAATGATGAGAGGCTGGCTCCAGAGGAGGAGGAGGAGG 2684
Db 2625 AGGGAATCCAAATGTTTATTAATGATGAGAGGCTGGCTCCAGAGGAGGAGGAGGAGG 2580
OY 2521 ACTTTGATGCGGACCGCAGGCTGCTCCAGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2744
Db 2685 ACTTTGATGCGGACCGCAGGCTGCTCCAGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2640
OY 2581 ACTGGAAGTCAAGATCATCTGACAGATTTGTAAGGAGGAGGAGGAGGAGGAGGAGG 2804
Db 2745 ACTGGAAGTCAAGATCATCTGACAGATTTGTAAGGAGGAGGAGGAGGAGGAGGAGG 2667
OY 2641 AGCTTGGCTCATGTCAAACTGAATTA 2831
Db 2805 AGCTTGGCTCATGTCAAACTGAATTA 2831

RESULT 4
AA14652 standard: cDNA: 2694 BP.
ID AA14652
AC AA14652:
XX 18-DEC-2001 (first entry)
DT Human cDNA encoding a voltage gated potassium channel hKvNO5-1.
DE Human cDNA encoding a voltage gated potassium channel hKvNO5-1.
XX Human: ss: voltage-gated potassium channel; hKvNO5-1; nootropic;
KW cerebroprotective; neurotropic; analgesic; migraine; hearing disorder;
KW central nervous system disorder; epilepsy; migraine; memory disorder;
KW psychotic disorder; seizure; learning disorder; memory disorder;
KW stroke; pain; gene therapy; splice variant.

```
XX Homo sapiens.
XX Key Location/Qualifiers
XX FT 1..2994
XX CDS /*tag= a
FT /product= "hKCN05-1"
XX
XX WO200170759-A1.
XX
XX 27-SEP-2001.
XX
XX 20-MAR-2001; 2001WO-US09328.
XX
XX 21-MAR-2000; 2000US-190954P.
XX
XX (ICAG-) ICAGEN INC.
XX
XX Jegla TJ;
XX
XX WPI: 2001-611467/70.
XX
XX P-PSDB; AAU09020.
XX
XX Polypeptides and polynucleotides of potassium channel KCNQ5 for
XX identifying a compound modulating ion flux in eukaryotic cell or cell
XX membrane expressing the protein, comprises KCNQ alpha
XX subunits
XX
XX Claim 5; Page 62-63; 78pp; English.
XX
XX The invention relates to an isolated polypeptide comprising an
XX alpha-subunit of a KCNQ potassium channel, with a subsequence having
XX 65% sequence identity to amino acids 343-640 of hKCN05-1 amino acid
XX sequence and forms a KCNQ potassium channel having the characteristic of
XX voltage-gating with at least an additional KCNQ alpha-subunit. Also
XX included in the scope of the invention are the nucleic acids encoding
XX hKCN05 (including splice variants encoding hKCN05-1 and hKCN05-2),
XX expression vectors encoding them, antibodies against them, the use of a
XX 3-dimensional computer modeling to identify molecules that bind to a
XX KCNQ containing potassium channel and modulate ion flux through the
XX channel. The KCNQ polypeptide is useful for identifying a compound that
XX increases or decreases ion flux through a potassium channel expressed in
XX an eukaryotic host cell or cell membrane. The compound (and the
XX KCNQ nucleic acid when used in gene therapy) is useful as
XX a pharmaceutical agent for treating diseases involving abnormal ion flux,
XX such as disorders of the central nervous system, such as epilepsy,
XX migraines, hearing and vision problems, psychotic disorders, seizures,
XX learning and memory disorders, stroke and pain. The antibodies are
XX useful for detecting a KCNQ5 polypeptide in a human tissue and the
XX use of a nucleotide sequence of KCNQ5 to search computer databases to
XX find variants of the sequence which are associated with disease states,
XX is useful for screening mutations of KCNQ5. The present sequence is
XX a splice variant of hKCN05 encoding hKCN05-1.
XX
XX Sequence 2694 BP: 714 A; 671 C; 669 G; 640 T; 0 other:
XX
XX Query Match 98.6%; Score 2630; DB 22; Length 2694;
XX Best Local Similarity 99.0%; Pred. No. 0;
XX Matches 2667; Conservative 0; Mismatches 0; Indels 27; Gaps 1;
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Db 181 TACACGAGTAGCCAGAGCTGCGGGCGCAACGTCACAGTACCGGGGTCAGAACTACCTG 240
OY 241 TACAACTGCTGAGAGAGACCCCGGGCTGGGGCTTCATCTACACAGCTTGGTTTTCG 300
Db 241 TACAACTGCTGAGAGAGACCCCGGGCTGGGGCTTCATCTACACAGCTTGGTTTTCG 300
OY 301 CTGTCCTTGGTGGTCTTATTTTGCAGTGTCTTACCATCTGAGCACAAATTTG 360
Db 301 CTGTCCTTGGTGGTCTTATTTTGCAGTGTCTTACCATCTGAGCACAAATTTG 360
OY 361 GCGTCAGTTGGCTCTTGATCTGCGAGTTCGATGATGTCTGCTTGGTTGAGTTG 420
Db 361 GCGTCAGTTGGCTCTTGATCTGCGAGTTCGATGATGTCTGCTTGGTTGAGTTG 420
OY 421 ATCATTTCCAAATCTGTCGCGGGGTTGCTGTGCAATATAGAGATGAGCAAGAGACTG 480
Db 421 ATCATTTCCAAATCTGTCGCGGGGTTGCTGTGCAATATAGAGATGAGCAAGAGACTG 480
OY 481 AGTTTGCATCGAAGACCCCTTGTGTATATAGATACCATTTGTTTATTCGCTTCAATAGCA 540
Db 481 AGTTTGCATCGAAGACCCCTTGTGTATATAGATACCATTTGTTTATTCGCTTCAATAGCA 540
OY 541 GTTGTCTTGCAGAAATCTGAGGTAATATTTTGGCAGCTTGCAGTCAAGAGTCCGT 600
Db 541 GTTGTCTTGCAGAAATCTGAGGTAATATTTTGGCAGCTTGCAGTCAAGAGTCCGT 600
OY 601 TTCTTACAGATCCCTCCGATGAGTGGCCATGAGACCGAAGGGAGGCACTGGAAATACAG 660
Db 601 TTCTTACAGATCCCTCCGATGAGTGGCCATGAGACCGAAGGGAGGCACTGGAAATACAG 660
OY 661 GGTTCAGTGGTTATGCTCAGACAGCAAGAAATTAATCAGACTTGTATAGAGATTTTGG 720
Db 661 GGTTCAGTGGTTATGCTCAGACAGCAAGAAATTAATCAGACTTGTATAGAGATTTTGG 720
OY 721 GTTCTTATTTTTCGTTCTTCTGTTCTATCTGCTGAGAAAGATGCCAATAAGATT 780
Db 721 GTTCTTATTTTTCGTTCTTCTGTTCTATCTGCTGAGAAAGATGCCAATAAGATT 780
OY 781 TCTACATATGACAGATCTCTCTGTTGGGCGACAAATTAATGCAACTATTTGGCTATGGA 840
Db 781 TCTACATATGACAGATCTCTCTGTTGGGCGACAAATTAATGCAACTATTTGGCTATGGA 840
OY 841 GACAAATCTCCCTAATCTGCTGAGAAATTTCTTTCTGACAGCTTGTGACCTCTTGGC 900
Db 841 GACAAATCTCCCTAATCTGCTGAGAAATTTCTTTCTGACAGCTTGTGACCTCTTGGC 900
OY 901 ATTCTTCTTCTTGCATCTCTGCGGATCTTGGCTCAGCTTTGCAATTAAGATACAA 960
Db 901 ATTCTTCTTCTTGCATCTCTGCGGATCTTGGCTCAGCTTTGCAATTAAGATACAA 960
OY 961 GAACAACACCGCCAGAAACCTTTGAGAAAAGAAAGAACCCAGCTGCAACCTATTCAG 1020
Db 961 GAACAACACCGCCAGAAACCTTTGAGAAAAGAAAGAACCCAGCTGCAACCTATTCAG 1020
OY 1021 TGTGTTTGGGCTAGTACGAGTATGAGAAATTTGTTTCCATTTGCACTGGAAGCCA 1080
Db 1021 TGTGTTTGGGCTAGTACGAGTATGAGAAATTTGTTTCCATTTGCACTGGAAGCCA 1080
OY 1081 CACTTGAAGGCTTGGCAGACCTGACGCTTACCA-- 1115
Db 1081 CACTTGAAGGCTTGGCAGACCTGACGCTTACCA-- 1115
OY 1116 -TCAGAGCTAAGTTTAAAGAGAGTCCGATGCTAGCCCCAGAGGGCCAGAGTATT 1173
Db 1116 -TCAGAGCTAAGTTTAAAGAGAGTCCGATGCTAGCCCCAGAGGGCCAGAGTATT 1173
OY 1141 AGTCAGAGCTAAGTTTAAAGAGAGTCCGATGCTAGCCCCAGAGGGCCAGAGTATT 1200
Db 1141 AGTCAGAGCTAAGTTTAAAGAGAGTCCGATGCTAGCCCCAGAGGGCCAGAGTATT 1200
OY 1174 AAGAGCCGACAAAGCTAGTAAAGTGAAGAGAGTCCCAAGCAGCAGATCAGAGCCGAG 1233
Db 1174 AAGAGCCGACAAAGCTAGTAAAGTGAAGAGAGTCCCAAGCAGCAGATCAGAGCCGAG 1233
OY 1201 AAGAGCCGACAAAGCTAGTAAAGTGAAGAGAGTCCCAAGCAGCAGATCAGAGCCGAG 1260
Db 1201 AAGAGCCGACAAAGCTAGTAAAGTGAAGAGAGTCCCAAGCAGCAGATCAGAGCCGAG 1260
OY 1234 GGCAGTCCCAAGTGAAGAGAGTGAAGTTCACAGCCGACCCGCTTCCGAGCC 1293
Db 1234 GGCAGTCCCAAGTGAAGAGAGTGAAGTTCACAGCCGACCCGCTTCCGAGCC 1293
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DB 1801 GCCTCAGCCCTCGCTTGGCTTCATTCAGATCCACCTTTTGAATGTGACAGACATCT 1860
OY 1834 GACTATCAAAAGCCCTGGTAGCAAGATCTTCGGGTCCGCGCAAAACAGTGGCTGC 1893
XX |||||||
DB 1861 GACTATCAAAAGCCCTGGTAGCAAGATCTTCGGGTCCGCGCAAAACAGTGGCTGC 1920
OY 1894 TTATCCAGATCACTAGTGCACATCTCGAGAGGCGCTGCATTCCTGACGCCAAAT 1953
XX |||||||
DB 1921 TTATCCAGATCACTAGTGCACATCTCGAGAGGCGCTGCATTCCTGACGCCAAAT 1980
OY 1954 GAGTTACGTCCCAAGACTTTCTACGCGCTTAGCCCTACTATGACAGTCAACACACAG 2013
XX |||||||
DB 1981 GAGTTACGTCCCAAGACTTTCTACGCGCTTAGCCCTACTATGACAGTCAACACACAG 2040
OY 2014 GTGCGCATTTAGTCAAAAGCGATGGCTCAGAGGCGCAGCCACACACATTCGAAACCAA 2073
XX |||||||
DB 2041 GTGCGCATTTAGTCAAAAGCGATGGCTCAGAGGCGCAGCCACACACATTCGAAACCAA 2100
OY 2074 ATAAATACGGCAGCCCAAGCGAGCGCCCAACACACTTACAGATCCACCTCTCTCCCA 2133
XX |||||||
DB 2101 ATAAATACGGCAGCCCAAGCGAGCGCCCAACACACTTACAGATCCACCTCTCTCCCA 2160
OY 2134 GCATCAGACATCTGCCAGGCGCAGAACTCGACCCCTACCCCTGAGGCTTACAGAA 2193
XX |||||||
DB 2161 GCCATCAGACATCTGCCAGGCGCAGAACTCGACCCCTACCCCTGAGGCTTACAGAA 2220
OY 2194 AGCATTTCTGACGTACACACCTGCTTGTGCTCCAGAAATTTGTCAGTTGACAG 2253
XX |||||||
DB 2221 AGCATTTCTGACGTACACACCTGCTTGTGCTCCAGAAATTTGTCAGTTGACAG 2280
OY 2254 TCAATATCTACCAAGAGACCGTTCTTAGAGAAAGCTTTGACATGGAGAGAGAACTCTG 2313
DB 2281 TCAATATCTACCAAGAGACCGTTCTTAGAGAAAGCTTTGACATGGAGAGAGAACTCTG 2340
OY 2314 TTGCTGTCTGTCCCATGAGTGCAGGAGGACTTGGCAATCTTTGTCTGTGCAAAACCTG 2373
DB 2341 TTGCTGTCTGTCCCATGAGTGCAGGAGGACTTGGCAATCTTTGTCTGTGCAAAACCTG 2400
OY 2374 ATCAGGTGACCCGAGAACTGATATATACACTTTTCAGGAGGTAGTCACTGGCTCCAGA 2433
DB 2401 ATCAGGTGACCCGAGAACTGATATATACACTTTTCAGGAGGTAGTCACTGGCTCCAGA 2460
OY 2434 GGCAGCCAGATTTTACCCTCCCAATGAGAGGAATCCAAATTTGTTTAACTGATGAAGAG 2493
DB 2461 GGCAGCCAGATTTTACCCTCCCAATGAGAGGAATCCAAATTTGTTTAACTGATGAAGAG 2520
OY 2494 GTGGGTCCCGAGAGACAGACACACTTTTGTATGCGCACCGACCGCTGCCAGGGAA 2553
DB 2521 GTGGGTCCCGAGAGACAGACACACTTTTGTATGCGCACCGACCGCTGCCAGGGAA 2580
OY 2554 GCTGCGTTTGCATCGACTCTCTTAAGAGCTGGAAGGTCAAGATCATCTCAGAGCATTTGT 2613
DB 2581 GCTGCGTTTGCATCGACTCTCTTAAGAGCTGGAAGGTCAAGATCATCTCAGAGCATTTGT 2640
OY 2614 AAGCAGAGAGAAAGTACAGATGCCCTCAGCTTGCTCATGTCAAACTGAATAATA 2667
DB 2641 AAGCAGAGAGAAAGTACAGATGCCCTCAGCTTGCTCATGTCAAACTGAATAATA 2694
XX |||||||
RESULT 6
AAS14651
ID AAS14651 standard; cDNA; 3071 BP.
XX
XX AAS14651;
XX
XX 18-DEC-2001 (first entry)
XX
XX Human cDNA for voltage gated potassium channel hKCNQ5.
DE
KW Human; ss; voltage-gated potassium channel; hKCNQ5; nootropic;
KW cerebroprotective; neurotropic; analgesic; vision disorder;
KW central nervous system disorder; epilepsy; migraine; hearing disorder;
KW psychotic disorder; seizure; learning disorder; memory disorder;
KW

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KW stroke; pain; gene therapy.
XX
XX Homo sapiens.
OS
XX WO200170759-A1.
PN
XX
XX 27-SEP-2001.
PD
XX
XX 20-MAR-2001; 2001WO-US09328.
PF
XX
XX 21-MAR-2000; 2000US-190954P.
PR
XX
XX (ICAG-) ICAGEN INC.
PA
XX
XX Jega1 TJ;
PI
XX
XX WPI; 2001-611467/70.
DR
XX
PT Polypeptides and polynucleotides of potassium channel KCNQ5 for
PT identifying a compound modulating ion flux in eukaryotic cell or cell
PT membrane expressing the protein, comprises KCNQ alpha
PT subunits
PT
XX
XX Claim 5; Page 61-62; 78pp; English.
PS
XX
CC The invention relates to an isolated polypeptide comprising an
CC alpha-subunit of a KCNQ potassium channel, with a subsequence having
CC 65% sequence identity to amino acids 343-640 of hKCNQ5-1 amino acid
CC sequence and forms a KCNQ potassium channel having the characteristic of
CC voltage-gating with at least an additional KCNQ alpha-subunit. Also
CC included in the scope of the invention are the nucleic acids encoding
CC hKCNQ5 (including splice variants encoding hKCNQ5-1 and hKCNQ5-2),
CC expression vectors encoding them, antibodies against them, the use of a
CC 3-dimensional computer modelling to identify molecules that bind to a
CC KCNQ containing potassium channel and modulate ion flux through the
CC channel. The KCNQ polypeptide is useful for identifying a compound that
CC increases or decreases ion flux through a potassium channel expressed in
CC an eukaryotic host cell or cell membrane. The compound (and the
CC KCNQ nucleic acid when used in gene therapy) is useful as
CC a pharmaceutical agent for treating diseases involving abnormal ion flux,
CC such as disorders of the central nervous system, such as epilepsy,
CC migraines, hearing and vision problems, psychotic disorders, seizures,
CC learning and memory disorders, stroke and pain. The antibodies are
CC useful for detecting a KCNQ5 polypeptide in a human tissue and the
CC use of a nucleotide sequence of KCNQ5 to search computer databases to
CC find variants of the sequence which are associated with disease states,
CC is useful for screening mutations of KCNQ5. The present sequence is
CC a representative cDNA for hKCNQ5.
CC
XX
XX

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Sequence 3071 BP; 849 A; 734 C; 737 G; 750 T; 1 other:

Query Match 98.5%; Score 2626.4; DB 22; Length 3071;
 Best Local Similarity 98.9%; Pred. No. 0;
 Matches 2664; Conservative 1; Mismatches 2; Indels 27; Gaps 1;

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OY 1 ATGAAGATGTGAGTGGCGCGGCGGCAAGGCTGCTGCTGAATCGGCGACGCCAGGGGC 60
DB 10 ATGAAGATGTGAGTGGCGCGGCGGCGGCAAGGCTGCTGCTGAATCGGCGACGCCAGGGGC 69
OY 61 GAGGCGCTGTACTGCTGGGCGACCGCGGCGGCGCAAGCTTGTGGGCGGCGGCGGCTGCT 120
DB 70 GAGGCGCTGTACTGCTGGGCGACCGCGGCGGCGCAAGCTTGTGGGCGGCGGCGGCTGCT 129
OY 121 AGGAGAGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCTGCT 180
DB 130 AGGAGAGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCTGCT 189
OY 181 TACACGAGTAGCCAGACCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCTG 240
DB 190 TACACGAGTAGCCAGACCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCTG 249
OY 241 TACACGAGTAGCCAGACCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCTG 300
DB |||||||

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Db 250 TACAACGTGCTGGAGAGACCCGCGGCTGGGCGTCACTACACCGCTTTCGTTTTCTC 309
OY 301 CTGTGCTTGGTGGCTGATTTTGTTCAGTCTTTTACCACTCCCTGAGCAGCAAAATTTG 360
Db 310 CTGTGCTTGGTGGCTGATTTTGTTCAGTCTTTTACCACTCCCTGAGCAGCAAAATTTG 369
OY 361 GCGCTAAGTGGCTCTGTATGCTGGAGTTCGTGATGATTCGTCCTTGGTTGGAGTTC 420
Db 370 GCGCTAAGTGGCTCTGTATGCTGGAGTTCGTGATGATTCGTCCTTGGTTGGAGTTC 429
OY 421 ATCATTTGGAATCTGCTGCGGGTTCCTGTTGTCATATAGAGANTGGCAAGAAGCTG 480
Db 430 ATCATTTGGAATCTGCTGCGGGTTCCTGTTGTCATATAGAGANTGGCAAGAAGCTG 489
OY 481 AGGTTGGCTCGAAGCGCTTCGTGTTATAGATACCATGCTGCTTATCGGTCATAGCA 540
Db 490 AGGTTGGCTCGAAGCGCTTCGTGTTATAGATACCATGCTGCTTATCGGTCATAGCA 549
OY 541 GTTGTTCGCAAAAACCTAGGGTAATATTTTGGCAGCTCTGCATCAGAAAGTCTCGT 600
Db 550 GTTGTTCGCAAAAACCTAGGGTAATATTTTGGCAGCTCTGCATCAGAAAGTCTCGT 609
OY 601 TTCTACAGATCTCTCCGATGTTGGCATGACCGAAGGGAGGCACTTGGAAATTTACTG 660
Db 610 TTCTACAGATCTCTCCGATGTTGGCATGACCGAAGGGAGGCACTTGGAAATTTACTG 669
OY 661 GGTTCAGTGGTTATGCTCACAGCAAGGAATTAATCAGCTGGTGCATGAGATTTTGTG 720
Db 670 GGTTCAGTGGTTATGCTCACAGCAAGGAATTAATCAGCTGGTGCATGAGATTTTGTG 729
OY 721 GTTCTATTTTTCGTCCTTTCCTTGTATCTGGTGGAAAAAGATGGCAATTAAGATTT 780
Db 730 GTTCTATTTTTCGTCCTTTCCTTGTATCTGGTGGAAAAAGATGGCAATTAAGATTT 789
OY 781 TCTACATATGAGATGCTCTGCTGGGGGCACAATTTACATTTGACATATGGCTATGGA 840
Db 790 TCTACATATGAGATGCTCTGCTGGGGGCACAATTTACATTTGACATATGGCTATGGA 849
OY 841 GACAAACCTCCCTAAGTTGGTGGGAAGATTCCTTCTGAGGCTTTCGACTCCTTGGC 900
Db 850 GACAAACCTCCCTAAGTTGGTGGGAAGATTCCTTCTGAGGCTTTCGACTCCTTGGC 909
OY 901 ATTTCTTTTTCGACTTCTGCGCGGATTCCTTGGCTCAGSTTTTGCATTAAGATACAA 960
Db 910 ATTTCTTTTTCGACTTCTGCGCGGATTCCTTGGCTCAGSTTTTGCATTAAGATACAA 969
OY 961 GAACACACCGCCAGAAACATTTGAAAAAAGAAAGAACCCAGTCCCAACCTCATTCAG 1020
Db 970 GAACACACCGCCAGAAACATTTGAAAAAAGAAAGAACCCAGTCCCAACCTCATTCAG 1029
OY 1021 TGTGTTGGGGTGGTTCAGAGCTGATGAGAAATCTGTTTCCATTTGCAACCTGGAAGCA 1080
Db 1030 TGTGTTGGGGTGGTTCAGAGCTGATGAGAAATCTGTTTCCATTTGCAACCTGGAAGCA 1089
OY 1081 CACTTGAAGGCTTTGACACCTGACGCCCTACAA----- 1115
Db 1090 CACTTGAAGGCTTTGACACCTGACGCCCTACAAAGAAAGAAAGGGAAGCATCAAGC 1149
OY 1116 --TCAGAAAGTAAGTTTAAGAGAGAGAGTGGCAATGCTAGCCCCAGGGGCGAGAGTAT 1173
Db 1150 AGTCAGAGGCTAAAGTTTAAAGAGAGAGTGGCAATGCTAGCCCCAGGGGCGAGAGTAT 1209
OY 1174 AAGAGCGCAAGAGCTCAGTAGGTGACAGAGAGGTCCCAAGACCCAGATCAGACCGAG 1233
Db 1210 AAGAGCGCGAAGAGCTCAGTAGGTGACAGAGAGGTCCCAAGACCCAGATCAGACCGAG 1269
OY 1234 GGCAGTCCCAAGAGTGCAGAAAGCTGAGCTTCAACGACCGAACCCTTCGCGGCC 1293
Db 1270 GGCAGTCCCAAGAGTGCAGAAAGCTGAGCTTCAACGACCGAACCCTTCGCGGCC 1329
OY 1294 TCGGTGGCCCAAAAGTTCACAGCAAAACAGATAGATGTGACACACCCCTTTGGC 1353
Db 1330 TCGGTGGCCCTCAAAAGTTCACAGCAAAACAGATAGATGTGACACACCCCTTTGGC 1389

OY 1354 ACTGATGATGTATATGATGAAAAAGAGATCCAGTGTGATGTATCAGTGGAGACCTCAC 1413
Db 1390 ACTGATGATGTATATGATGAAAAAGAGATCCAGTGTGATGTATCAGTGGAGACCTCAC 1449
OY 1414 CCACCACTTAAACTGTCTATTTGAGCTATACAGATTTATGAAATTTTATGTTGCAAAACG 1473
Db 1450 CCACCACTTAAACTGTCTATTTGAGCTATACAGATTTATGAAATTTTATGTTGCAAAACG 1509
OY 1474 AAGTTTAAGGAAGCTTACGTCCATGTAGTGTAAAGAGTGCATTAACATATTTGCT 1533
Db 1510 AAGTTTAAGGAAGCTTACGTCCATGTAGTGTAAAGAGTGTCTTTGAACATATTTGCT 1569
OY 1534 GGTCAATCTGGACATGTTGTAGAAATTTAAAGCCTTCAACACGTGTGATCAAAATCTT 1593
Db 1570 GGTCAATCTGGACATGTTGTAGAAATTTAAAGCCTTCAACACGTGTGATCAAAATCTT 1629
OY 1594 GGAAGAGGCAAAATCATCATCAGATTAAGAAAGCGGAGAGAAAAATTAACAGACAACTGAG 1653
Db 1630 GGAAGAGGCAAAATCATCATCAGATTAAGAAAGCGGAGAGAAAAATTAACAGACAACTGAG 1689
OY 1654 ACCACAGAGATCTGATAGTGTGCGGTGCGGTGTCAGAGTTGAAAAACAGTACAGTCC 1713
Db 1690 ACCACAGAGATCTGATAGTGTGCGGTGCGGTGTCAGAGTTGAAAAACAGTACAGTCC 1749
OY 1714 ATAGAGTCCCAAGCTGAGCTGCTTACTAGACATCTATCAACAGGTCTTGGAAAGGCTCT 1773
Db 1750 ATAGAGTCCCAAGCTGAGCTGCTTACTAGACATCTATCAACAGGTCTTGGAAAGGCTCT 1809
OY 1774 GCTTCAGCCCTGCTTGGCTTATTCAGATTCACACCTTTTGAATGTGAACAGACATCT 1833
Db 1810 GCTTCAGCCCTGCTTGGCTTATTCAGATTCACACCTTTTGAATGTGAACAGACATCT 1869
OY 1834 GACTATCAAGCCCTGCTGATAGCAAAAGATCTTGGGTTCCGACAAACAGTGGCTGC 1893
Db 1870 GACTATCAAGCCCTGCTGATAGCAAAAGATCTTGGGTTCCGACAAACAGTGGCTGC 1929
OY 1894 TTATCCAGATCAACTGATGCGCAACATCTGAGAGGCTGCAATTTGAAAGTGAACACATCT 1933
Db 1930 TTATCCAGATCAACTGATGCGCAACATCTGAGAGGCTGCAATTTGAAAGTGAACACATCT 1989
OY 1954 GAGTTAGGCGCCAGATTTCTACGGGCTTAAGCCCTCTATGCAAGTCAAGCAAGCAG 2013
Db 1990 GAGTTAGGCGCCAGATTTCTACGGGCTTAAGCCCTCTATGCAAGTCAAGCAAGCAG 2049
OY 2014 GTGCCAATTAGTCAAAAGCGATGCTCAGAGTGGCAGCCCAACACCATTTGCAAAACCA 2073
Db 2050 GTGCCAATTAGTCAAAAGCGATGCTCAGAGTGGCAGCCCAACACCATTTGCAAAACCA 2109
OY 2074 ATTAATTAAGGCAACCAAGCAGACGCCCCCAACAATTATACAGATCCACTCTCTCCCA 2133
Db 2110 ATTAATTAAGGCAACCAAGCAGACGCCCCCAACAATTATACAGATCCACTCTCTCCCA 2169
OY 2134 GGCATTAAGATCTGCGCCAGGCAAGAAAGTCTGACCTTAACCTGCAAGGCTTACAGGAA 2193
Db 2170 GGCATTAAGATCTGCGCCAGGCAAGAAAGTCTGACCTTAACCTGCAAGGCTTACAGGAA 2229
OY 2194 AGCATTTCTGACGTCACACACTGCTTGTTCCTCAAGGAAATGTTCAAGTTGACAG 2253
Db 2230 AGCATTTCTGACGTCACACACTGCTTGTTCCTCAAGGAAATGTTCAAGTTGACAG 2289
OY 2254 TCAAAATCTCAACGAAGACGCTTCTATAGAGAAAGCTTTGACATGGGAGGAAACCTGT 2313
Db 2290 TCAAAATCTCAACGAAGACGCTTCTATAGAGAAAGCTTTGACATGGGAGGAAACCTGT 2349
OY 2314 TTGTCTGTCTGCTCCATGAGTGGCCGAAGACTTGGGCAAAATCTTTGTCTGCAAAACCTG 2373
Db 2350 TTGTCTGTCTGCTCCATGAGTGGTCCGAAGACTTGGGCAAAATCTTTGTCTGCAAAACCTG 2409
OY 2374 ATCAGGTGACCGAGAGAACTGAATATACACTTTCAGGAGTGAAGTGAAGTGGCTCCAGA 2433
Db 2410 ATCAGGTGACCGAGAGAACTGAATATACACTTTCAGGAGTGAAGTGAAGTGGCTCCAGA 2469

OY	2434	GGAGCCAGCATTTTAAACCCCAATGAGGAGATCCAAATGTTTATACGTATGAAGAG	2493
OY	2434	GGAGCCAGCATTTTAAACCCCAATGAGGAGATCCAAATGTTTATACGTATGAAGAG	2493
Db	2470	GGAGCCAGCATTTTAAACCCCAATGAGGAGATCCAAATGTTTATACGTATGAAGAG	2529
OY	2494	GTCGGTCCCGAAGAGACAGACAGACACTTTTGATGCGCCAGCCGAGCCTGCCAGGAA	2553
Db	2530	GTCGGTCCCGAAGAGACAGACAGACACTTTTGATGCGCCAGCCGAGCCTGCCAGGAA	2589
OY	2554	GCTGCTTTGCATCAGACTCTCTAAGAGCTGAAGGTCAAGATCATCTCAGACATTGT	2613
Db	2590	GCTGCTTTGCATCAGACTCTCTAAGAGCTGAAGGTCAAGATCATCTCAGACATTGT	2649
OY	2614	AAGCAGAGGAAGATCAGATGCGCTCAGCTTGCCCTCATGTCAACTGAATAA	2667
Db	2650	AAGCAGAGGAAGATCAGATGCGCTCAGCTTGCCCTCATGTCAACTGAATAA	2703
RESULT 7			
AAC85414			
ID	AAC85414	standard; cDNA; 3137 BP.	
XX			
AC	AAC85414;		
DT	20-APR-2001	(first entry)	
XX			
DE	Human KCNQ5 potassium channel subunit coding sequence.		
XX			
KM	Human; KCNQ5; heteromeric channel; chromosome 6; Parkinson's disease;		
KM	central nervous system; CNS; Alzheimer's disease; anxiety; ataxia;		
KM	CNS damage; trauma; stroke; neurodegenerative illness; schizophrenia;		
KM	compulsive behaviour; dementia; depression; Huntington's disease;		
KM	mania; memory impairment; memory dysfunction; spinal cord damage;		
KM	phobia; pick's disease; psychosis; stroke; tremor; seizure; convulsion;		
KM	epilepsy; ds.		
XX			
OS	Homo sapiens.		
XX			
FH	Key	Location/Qualifiers	
FT	CDS	1..2694	
FT		/*tag= a	
FT		/product= "KCNQ5 subunit"	
PN	W0200077035-A2.		
PD			
XX	21-DEC-2000.		
XX	29-MAY-2000; 2000WO-DK00289.		
XX	11-JUN-1999; 99DK-0000828.		
XX	(NEUR-) NEUROSEARCH AS.		
PA			
PI	Jentsch TJ;		
DR	WPI; 2001-080678/09.		
DR	P-PSDB; AAB47046.		
XX			
CC	This sequence encodes the human KCNQ5 protein. The KCNQ5 protein forms heteromeric channels with other KCNQ channel subunits, in particular KCNQ3 and KCNQ4. The KCNQ5 gene has been localised to the long arm of chromosome 6 (6p14). Chemicals which have the ability to bind to KCNQ5 are useful for diagnosis, treatment, prevention or alleviation of diseases related to diseases or adverse conditions of the central nervous system (CNS), including affective disorders, Alzheimer's disease, anxiety, ataxia, CNS damage caused by trauma, stroke or neurodegenerative illness, cognitive deficits, compulsive behavior.		
CC	Claim 2; Page 44-48; 50pp; English.		

	CC	dementia, depression, Huntington's disease, mania, memory impairment,
	CC	memory disorders, memory dysfunction, motion disorders, motor
	CC	disorders, neurodegenerative diseases, Parkinson's disease and
	CC	Parkinson-like motor disorders, phobias, pick's disease, psychosis,
	CC	schizophrenia, spinal cord damage, stroke, tremor, seizures,
	CC	convulsions and epilepsy.
XX	Sequence	3137 BP; 865 A; 749 C; 745 G; 778 T; 0 other;
SQ	Query Match	98.4%; Score 2625; 2; DB 22; Length 3137;
	Best Local Similarity	98.9%; Pred. No. 0;
	Matches 2664;	Conservative 0; Mismatches 3; Indels 27; Gaps 1;
OY	1	ATGAAGATGTGAGTGGGCCGGGCAGAGGATGCTGCTAACTCGCAGCCGCAAGGGC 60
Db	1	ATGAAGATGTGAGTGGGCCGGGCAGAGGATGCTGCTAACTCGCAGCCGCAAGGGC 60
OY	61	GAGGCGCTGCTACTGCTGGGACACC GGCGCCGACGCTTGTTGGCGGGCGGCTG 120
Db	61	GAGGCGCTGCTACTGCTGGGACACC GGCGCCGACGCTTGTTGGCGGGCGGCTG 120
OY	121	AGGAGAGACCGCCGGGGCAAGCAGAGGGCCCGGATGAGCTCTGGGAGAACCGCTCT 180
Db	121	AGGAGAGACCGCCGGGGCAAGCAGAGGGCCCGGATGAGCTCTGGGAGAACCGCTCT 180
OY	181	TACACGATGACCAAGAGCTGCCGGCGCAACGTCAAGTACCGGGGGTCAGAACTACTG 240
Db	181	TACACGATGACCAAGAGCTGCCGGCGCAACGTCAAGTACCGGGGGTCAGAACTACTG 240
OY	241	TACAACGTGTGAGAGACCCGGCGGGGGGTCACTACACAGCTTGCTTTTC 300
Db	241	TACAACGTGTGAGAGACCCGGCGGGGGGTCACTACACAGCTTGCTTTTC 300
OY	301	CTTGCTCTTGGTTCCTGATTGTTGCTAGTGGTTTTCTACCATCCGTGAGCACAAAAATTG 360
Db	301	CTTGCTCTTGGTTCCTGATTGTTGCTAGTGGTTTTCTACCATCCGTGAGCACAAAAATTG 360
OY	361	GCTCAAGTGGCCTCTGATATCTGAGTTCGTGATGTTGTCGTTGGTTGGATTC 420
Db	361	GCTCAAGTGGCCTCTGATATCTGAGTTCGTGATGTTGTCGTTGGTTGGATTC 420
OY	421	ATCATTGGAATCTGCTGCGGGGTTGCTTTGTCGATATAGAGATGGCAAGAAGACTG 480
Db	421	ATCATTGGAATCTGCTGCGGGGTTGCTTTGTCGATATAGAGATGGCAAGAAGACTG 480
OY	481	AGGTTGTCGCGAAGCCCTCTGCTTATATAGATACATTTGTTCTTATGCTTCAATAGA 540
Db	481	AGGTTGTCGCGAAGCCCTCTGCTTATATAGATACATTTGTTCTTATGCTTCAATAGA 540
OY	541	GTTGTTTCGCAAAAACCTCAGGTAATAATTTTCCACGTCGTGCACCTAGAGTCTCCGT 600
Db	541	GTTGTTTCGCAAAAACCTCAGGTAATAATTTTCCACGTCGTGCACCTAGAGTCTCCGT 600
OY	601	TTCCTTACAGATCCTCCGCATGCTGCGCATGAGACCGAAGGGGACACTTGGAAATTACTG 660
Db	601	TTCCTTACAGATCCTCCGCATGCTGCGCATGAGACCGAAGGGGACACTTGGAAATTACTG 660
OY	661	GGTTCAGTGGTATATGCTCACAGCAAGAAATTAATCAGCTTGATATAGATTTTGG 720
Db	661	GGTTCAGTGGTATATGCTCACAGCAAGAAATTAATCAGCTTGATATAGATTTTGG 720
OY	721	GTTCTATTATTTTGGTCTTCCCTGTTCTATCTGCTGGAAGAAAGATGCCAAATAAGATT 780
Db	721	GTTCTATTATTTTGGTCTTCCCTGTTCTATCTGCTGGAAGAAAGATGCCAAATAAGATT 780
OY	781	TCTACATTAGCAGATCTCTCTGTTGGGCAATTAATCATTTGACAACTATTGGCTATGA 840
Db	781	TCTACATTAGCAGATCTCTCTGTTGGGCAATTAATCATTTGACAACTATTGGCTATGA 840
OY	841	GACAAAGTCCCCCTACTTGGCTGGGAAATTCCTTCTGAGGCTTTGCACCTCTTGGC 900
Db	841	GACAAAGTCCCCCTACTTGGCTGGGAAATTCCTTCTGAGGCTTTGCACCTCTTGGC 900

Db	1835	GGAAAAAGGCAATTCATCATCATTAAGAAAGACCCAGAAAAATATACGACGAAACATBAG	1894
QY	1654	ACCACAGACGATCTCAGTATGCTCGGTGGGTGTCAAAGTTGAAAAACAGGTACAGTCC	1713
Db	1895	ACCACAGACGATCTCAGTATGCTCGGTGGGTGTCAAAGTTGAAAAACAGGTACAGTCC	1954
QY	1714	ATAGAGTCGCAAGTGGAGTGGCTTACTAGACATCTATCAACAGTCCCTCGGAAAGGCTCT	1773
Db	1955	ATAGAAATCCAAAGTGGAGTGGCTTACTAGACATCTATCAACAGTCCCTCGGAAAGGCTCT	2014
QY	1774	GCCTCAGACCCCTCGCTTTGGCTTCATCTCCAGATCCCAACCTTTTGAATGTGAACAGACATCT	1833
Db	2015	GCCTCAGACCCCTCGCTTTGGCTTCATCTCCAGATCCCAACCTTTTGAATGTGAACAGACATCT	2074
QY	1834	GACTATCAAAAGCCCTGTGCATAGCAAAAGATCTTTTGGGCTTCGGCACAAACAGTGGCTGC	1893
Db	2075	GACTATCAAAAGCCCTGTGCATAGCAAAAGATCTTTTGGGCTTCGGCACAAACAGTGGCTGC	2134
QY	1894	TTATATCAGATCACTAGTGGCAACATCTGSAAGGGCTTCAGTTCACTCTGACGCCAAT	1953
Db	2135	TTATATCAGATCACTAGTGGCAACATCTGSAAGGGCTTCAGTTCACTCTGACGCCAAT	2194
QY	1954	GAGTCAGTGGCCGACACTTCTTAACGGCTTACCCTTACTATGSCACAGTCAAGCAACACAG	2013
Db	2195	GAGTCAGTGGCCGACACTTCTTAACGGCTTACCCTTACTATGSCACAGTCAAGCAACACAG	2254
QY	2014	GTGCGAATTGTGTAAGGCATGGCTGTAGAGATGGCAAGCCACCAACCATTTGCCAACCA	2073
Db	2255	GTGCGAATTGTGTAAGGCATGGCTGTAGAGATGGCAAGCCACCAACCATTTGCCAACCA	2314
QY	2074	ATTAATTCGCGACCCCAAGCAGAGAGCCCAACAACTTTACAGATCCCACTTCCTCCCA	2133
Db	2315	ATTAATTCGCGACCCCAAGCAGAGAGCCCAACAACTTTACAGATCCCACTTCCTCCCA	2374
QY	2134	GCCATCAGCATGTGCCCAGGCCAAGAACTCTGCACCTTAACCTTCGACGCTTACAGAA	2193
Db	2375	GCCATCAGCATGTGCCCAGGCCAAGAACTCTGCACCTTAACCTTCGACGCTTACAGAA	2434
QY	2194	AGCATTTCTCAGCGCACACACACTGCTTGTGGCTCCAAAGAAAATGTTACAGTTGCACAG	2253
Db	2435	AGCATTTCTCAGCGCACACACACTGCTTGTGGCTCCAAAGAAAATGTTACAGTTGCACAG	2494
QY	2254	TCAAAATCTCAACCAAGACGCTTCTATAGAGAAAAGCTTTGACATGGGAGACAGAACTCTG	2313
Db	2495	TCAAAATCTCAACCAAGACGCTTCTATAGAGAAAAGCTTTGACATGGGAGACAGAACTCTG	2553
QY	2314	TTGTGCTGTGTCGCCCATGGGCGGGAAGGACTTGGGCAATCTTTGTCTGTGTGCAAAACCTG	2373
Db	2555	TTGTGCTGTGTCGCCCATGGGCGGGAAGGACTTGGGCAATCTTTGTCTGTGTGCAAAACCTG	2614
QY	2374	ATCAGGTGCAAGCAGAGAACTGAATATACAATTTACAGGAGTGAAGTCAAGTGGCTCCAGA	2433
Db	2615	ATCAGGTGCAAGCAGAGAACTGAATATACAATTTACAGGAGTGAAGTCAAGTGGCTCCAGA	2674
QY	2434	GCGACGCCAATTTTAACTCCCAATATGGAGGGAATCCAAATTTGTTATTAACATGAAGAAG	2493
Db	2675	GCGACGCCAATTTTAACTCCCAATATGGAGGGAATCCAAATTTGTTATTAACATGAAGAAG	2734
QY	2494	GTGGGTCGCCCAAGACAGACAGACACACTTTTGTATGCCGACCCGACGCTCCACAGGAA	2553
Db	2735	GTGGGTCGCCCAAGACAGACAGACACACTTTTGTATGCCGACCCGACGCTCCACAGGAA	2794
QY	2554	GCTGCCCTTGTGATCAGACTCTCTTAAGAGCTGGAAGGTCAAGTCAATCTCAGACATTTGT	2613
Db	2795	GCTGCCCTTGTGATCAGACTCTCTTAAGAGCTGGAAGGTCAAGTCAATCTCAGACATTTGT	2854
QY	2614	AAGCAGAGAGAAAGTACAGATGGCTCAGCTTCCCTCAATGTCAAACTGAAATAA 2667	
Db	2855	AAGCAGAGAGAAAGTACAGATGGCTCAGCTTCCCTCAATGTCAAACTGAAATAA 2908	
RESULT 9			

[illegible]

Db	258	TTGATGTACCAAGCCTTTGCTTTTCTCCTGCTCTTTGGTTGCTGTGATTTTGTCAAGTCTTT	317
Qy	334	TCGTACATCCCTGAGGACACACAAATTTGGCCTCAAGTTGGCTCTTGATCTCGAGTTGGT	393
Db	318	TCGTACATCCCTGAGGACACACAAATTTGGCCTCAAGTTGGCTCTTGATCTCGAGTTGGT	377
Qy	394	ATGATTTGTGCTTTTGGTTTGGAGTTTCATTCGGAATCTGTGCTCGGGTGTGCTTTGT	453
Db	378	ATGATTTGTGCTTTTGGTTTGGAGTTTCATTCGGAATCTGTGCTCGGGTGTGCTTTGT	437
Qy	454	CGATATAGAGGATGGGCAAGAGACTGAGGTTTGGTCGGAAGCCCTCTGTATATGAT	513
Db	438	CGATATAGAGGATGGGCAAGAGACTGAGGTTTGGTCGGAAGCCCTCTGTATATGAT	497
Qy	514	ACCATTTGTTCTTATCCGCTTCAATAGCAGTTGTTTGTGCAAAAACCTCAGGGTAATATTTT	573
Db	498	ACCATTTGTTCTTATCCGCTTCAATAGCAGTTGTTTGTGCAAAAACCTCAGGGTAATATTTT	557
Qy	574	GCCAGCTCTGCACTCGAAGTCTCCGTTTCTACAGATCTCCGATGTGGCCAGTGGAC	633
Db	558	GCCAGCTCTGCACTCGAAGTCTCCGTTTCTACAGATCTCCGATGTGGCCAGTGGAC	617
Qy	634	CGAAGGGGAGGCACTTGGAAATTAAGTGGGTTCAGTGGTTATGCTCACACAGAGAAATTA	693
Db	618	CGAAGGGGAGGCACTTGGAAATTAAGTGGGTTCAGTGGTTATGCTCACACAGAGAAATTA	677
Qy	694	ATCACAGCTTGGTACATAGAGATTTTGGTTCTTATTTTTCGTCTTCTCTGTCTATCTG	753
Db	678	ATCACAGCTTGGTACATAGAGATTTTGGTTCTTATTTTTCGTCTTCTCTGTCTATCTG	737
Qy	754	GTTGGAAGAAGATGCCAATAAAGATTTTCTACTATGACAGATGCTCTGTGGGGCACA	813
Db	738	GTTGGAAGAAGATGCCAATAAAGATTTTCTACTATGACAGATGCTCTGTGGGGCACA	797
Qy	814	ATTACATTGACAATTTATGCTATGAGACAAAACTCCCTAATTGGGCTGGGGAAGTTG	873
Db	798	ATTACATTGACAATTTATGCTATGAGACAAAACTCCCTAATTGGGCTGGGGAAGTTG	857
Qy	874	CTTTCTGCAAGGCTTTGCACTCCTTTGGCATTTCTTCTTGACATCTCTGCGGCATTTCT	933
Db	858	CTTTCTGCAAGGCTTTGCACTCCTTTGGCATTTCTTCTTGACATCTCTGCGGCATTTCT	917
Qy	934	GGCTCAGGTTTGGCATTTAAAGTACAAAGAACACCCGCCAGAAACATTTGAGAAAGA	993
Db	918	GGCTCAGGTTTGGCATTTAAAGTACAAAGAACACCCGCCAGAAACATTTGAGAAAGA	977
Qy	994	AGGAACCCAGCTGCAACCTCATTCAGTGTGTTGGCTAGTATGACGAGTGTATGAAA	1053
Db	978	AGGAACCCAGCTGCAACCTCATTCAGTGTGTTGGCTAGTATGACGAGTGTATGAAA	1037
Qy	1054	TCGTGTTTCATTGCAACCTTGGAAGCCATCTGGAAGCCCTGCAACCTGCAACCCCTTAC	1113
Db	1038	TCGTGTTTCATTGCAACCTTGGAAGCCATCTGGAAGCCCTGCAACCTGCAACCCCTTAC	1097
Qy	1114	AA-----TCAGAAGCTTAAGTTTAAAGACGAGTGGCG	1146
Db	1098	AAAGAAAGAAAGGAGGAAAGCATCAAGCAGTCAAGAACTTAAGTTTAAAGACGAGTGGCG	1157
Qy	1147	ATGGCTAGCCCCAGGGGCCAGAGATTTAGAGGCCGACAGCCCTCATAGGTGACAGAGG	1206
Db	1158	ATGGCTAGCCCCAGGGGCCAGAGATTTAGAGGCCGACAGCCCTCATAGGTGACAGAGG	1217
Qy	1207	TCGCCAAGCAGCATCAAGCCGAGGGCAGTCCCAACCAAGTGCAGAAAGACTGGAGC	1266
Db	1218	TCGCCAAGCAGCATCAAGCCGAGGGCAGTCCCAACCAAGTGCAGAAAGACTGGAGC	1277
Qy	1267	TTTCAAGCAGAACCCGCTTCCGGCCCTGCTGCGCCTCAAAAGTTCTCAGCCAAAACCA	1326
Db	1278	TTTCAAGCAGAACCCGCTTCCGGCCCTGCTGCGCCTCAAAAGTTCTCAGCCAAAACCA	1337
Qy	1327	GTGATATGATGCTGACACAGCCCTTGGCACTGATGATGTATATGATGAAAAAGATGCCAG	1386
Db	1338	GTGATATGATGCTGACACAGCCCTTGGCACTGATGATGTATGATGAAAAAGATGCCAG	1397

D	b	1100	ATGCGGAGGCAACCTCATCCAGGCTGGCTGGCGCTGACTCCACGATATGAGCGG	1159
Q	y	1057	GTTTCATTGCAACCTGGAAGCCACACTTTGAAAGCCTTGCACAC-----	1100
D	b	1160	GCCATACGTGACAGCCACCTGTACTACTATGTACAGATATCTCCATCTTCAGAGACTG	1219
Q	y	1101	-----	1100
D	b	1220	GCCCTCTGTTGAGCAGCTGCAAGGGGCCCAATGGGGGCTTACGGCCCTGGAGGTG	1279
Q	y	1101	-----	1100
D	b	1280	CGGCGGGGCGCGTACCCGAGGAGACCCCTCCCGTTACCCGGCCGTTGGCACTGGCAC	1339
Q	y	1101	-----CTGCAGCCCTTACCAATCAGAGCTAAGTTTAAAGAGCGA	1140
D	b	1340	CGGGCGGGCAGCACCTCTCTCTCCCTGGGGAAAGCAGCCCGATGGGCATCAAAAGCCG	1399
Q	y	1141	GTGGCATGGCTAGGCCCCCGGGGGCCAGAGATAT-----AAGAGCGACAAAGCCTCAGTA	1194
D	b	1400	ATCCGCAATGGCAGCTCCCGACGGCGGAGGGTCTTTCCAAAGCAGCAGCTGGCACTTCA	1458
Q	y	1195	GCTGCAGGAGGTTCCCAAGCAGCACCGACATCACAGCCGAG--GCAGTCCCAACAAAGTG	125D
D	b	1460	ACAATGCCCACTCCCGCAAGCAGGCGAGCAGGTGGTGGTAGGCCACACAGCCCAAGAGTG	1519
Q	y	1232	CAGAAGAGCTGACGCTTCAACAGCCAGCAACCCGCTTCGGCGCTTGGCTGCGCTCAAAAGT	1311
D	b	1520	CAAAAGAGTGGAGCTTCATGATCAAGCCACCCCGGCTTCCGGGCATCTCGAGACTC-----	1573
Q	y	1312	TCTCAGCCCAACCAAGTGTAGTGTGTGACACAGCCCTTGGCACTGATGTATGTATGAT	1371
D	b	1574	-----AAACCCCGCACCTCTGCTGAGAGATGCC---CTTCAGAGGAAGTATGACAGAG	1621
Q	y	1372	GAAAAAGATGCGCAGTGTGATGTATCAGTGGAGAGACCTCAACCCACCACTTAAACGTCTC	1431
D	b	1622	GAGAGAGCTACCACTGTGAGTGCACAGGTGGAGACATCATGCTGCTGTGAAACAGACTC	1681
Q	y	1432	ATTTCAGCTATCAGAAATTATGAAATTTTCATGTTGCCAAACGGGAAGTTTAAAGAAACGTTA	1491
D	b	1682	ATTCGCTCCATAGAGATTCTCAAGTTCTCTGTGGCCAAAGAAATTCAGAGAGACACTG	1741
Q	y	1492	CGTCCATATGATGTAAAGATGTCTATTTGAACAAATATTCTGCTGTCACTGGACATGTTG	1551
D	b	1742	CGACCGTACGAGTGGAAGCGCTCATTTGACAGTACAGAGAGCCACCTGGACATGCTG	1801
Q	y	1552	TGTAGCAATTAAGACCTTCAACACGCTGTGATCAATTTCTTGGAAAAAGGC---AATTC	1601
D	b	1802	GGCCGGATTAAGGCGCTGCAAACTCGGGTGGACCAAAATTTGGGGTGGGGGCCCGGGGAC	1861
Q	y	1609	ACATCAGATAGCAAGACCGGAGAGAAATAACAGCAACATGAGACACAGAGAGATTC	1666
D	b	1862	AGGAAGGCCCGGAGAAAGGCGCAAGGGGCCCTCGCAGCGGAGAGTGTGGATGAATTC	1922
Q	y	1669	AGTATGCTGCGTGGGTGCTGCAAGGTTGAAAAACAGGTACAGTCCATATGAGTCAAGCTG	1722
D	b	1922	ACCATGATGGAGCGCTGTGGTCAAGGTGGAGAAAGAGGTGCGTCCATCGACACACAGCTG	1981
Q	y	1729	GACTGCTACTAGACATCTATCAACAGAGTCCCTTGGGAAAGGCTCGGCTCAGACCCTGCT	1788
D	b	1982	GACCTGCTGTTGGGCTTCTATTTCGTGCGCTGCTGC-----GCTGTGGCACTCGGCCACG	2033
Q	y	1789	TTGGCTTCAATTCAGATCCCACTTTTGAATGTGAACAGACAGACTCTATCAAGCCCT	1848
D	b	2036	CTGGGGCGCGTGCAGAGTGCCTGTTTGACCCGACATCACTCCGACTTACCACAGCCCT	2091
Q	y	1849	GTGATAGCAAAATCTTTGGGTTCCGGCAAAA	1882
D	b	2096	GTGGACACGAGGACATCTCCGTTCCGCAAGA	2129

RESULT 12
AAX57140

ID	AAK57140 standard; DNA; 2273 BP.
XX	
AC	AAK57140:
XX	
DJ	22-JUL-1999 (first entry)
XX	
DE	Mouse KCNQ2 cDNA.
XX	
KW	KCNQ2; KCNQ3; human; murine; potassium channel; diagnosis; prognosis;
KM	benign familial neonatal epilepsy; BFNE; juvenile myotonic epilepsy;
KW	JME; rolandic epilepsy; mutant; treatment; screening; epilepsy;
KM	detection; gene therapy; drug screening; ss.
XX	
OS	Mus musculus.
XX	
FT	Key Location/Qualifiers
FT	CDS 1..2273
FT	/tag= a
FT	/product= "KCNQ2"
FT	/note= "Partial sequence, no stop codon given"
XX	
PN	MO9921875-A1.
XX	
PD	06-MAY-1999.
XX	
PF	23-OCT-1998; 98WO-US22375.
XX	
PR	24-OCT-1997; 97US-0063147.
XX	
PA	(UTAH) UNIV UTAH RES FOUND.
XX	
PI	Charlier C, Leppert MF, Singh NA;
XX	
DR	WPI: 1999-312938/26.
XX	
DR	P-PSDB: AAK08345.
XX	
PT	Nucleic acid encoding potassium channels KCNQ2 and 3
XX	
PS	Claim 1; Page 153-156; 195pp; English.
XX	
CC	This invention describes novel human and mouse potassium channel proteins KCNQ2 and KCNQ3. Detecting mutations in sequences that encode KCNQ2 or KCNQ3, or the loss of one copy of these genes, is used for diagnosis and prognosis of benign familial neonatal epilepsy (BFNE), juvenile myotonic epilepsy (JME) or rolandic epilepsy (RE). Cells (or transgenic animals) that express wild-type or mutant KCNQ2 or 3 (also the proteins themselves in cell-free form) are used to screen for agents that can be used to treat or prevent these forms of epilepsy. Fragments of the encoding nucleic acids are used as probes or primers, either for detecting mutations or for isolation of related sequences, while the complete sequences may be used in gene therapy to provide wild-type protein. Antibodies specific for mutant or wild-type proteins are used as diagnostic reagents and for drug screening. The KCNQ2 and 3 proteins are useful in rational design of drugs and therapeuticaly (in replacement therapies). The forms of epilepsy associated with mutations in KCNQ2 and 3 sequences can now be diagnosed early (before symptoms are manifest), and better treatment options will be available.
XX	
CC	
XX	
SO	Sequence 2273 BP; 486 A; 670 C; 653 G; 448 T; 16 other:
Query Match	18.3%; Score 489.2; DB 20; Length 2273;
Best Local Similarity	57.0%; Pred. No. 2,7e-133;
Matches 1020; Conservative	2; Mismatches 667; Indels 99; Gaps 4
QY	64 GGCCTGCTACTGCTGGGCAACCGCGCGCAGCTTGTCGTGGCGCGCGTGGCTGAGG 123
DB	67 GGCCTGCTGTTGCTGGATACCCTGGCGGCCGANTCCACACGCGAGCGCMNCNTACTCATC 126
QY	124 GAGAGCCGCGGGGGAAGAAGAGAGGGGCGCGAGTAGAGCTCTCTGGGGAAGCCGCTCTTAC 183
DB	127 GCGGGCTCCGAGAGCCCCCAAGCGCGGCANCMNTTTAGACAAGCGCGGAGACGGCGGCGG 186
QY	184 ACAGTAGCCAGAGCTGCCGCGCAACGTCAAGTACCGCGGGGTGTCAGACTACTCTGTAC 243

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Db 187 GGAGCCGGAGAGCCGCCAANAGCAAGCCTTCTACCGCAAGCTGAGATTTCTCTAC 246
QY 244 AACGTGCTGGAGAACCCCGGGCTGGGGCTTCACTACACAGCTTTCCTTCTT 303
Db 247 AACGTGCTGGAGAACCCCGGGCTGGGGCTTCACTACACAGCTTTCCTCTG 306
QY 304 GTCCTTGGTCTGATTTGTGATGTTTCTTCTACATCCCGAGACACCAAAATTGGCC 363
Db 307 GTTTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 366
QY 364 TCAAGTTGCTCTGATGCTGAGTTCGTATGATGTTGCTTCTTGGTGGAGTTCATC 423
Db 367 GAGGGGCGCTCTCACTCTGGAATCGTACTATCGTGTATCGTGTGAGTACTTT 426
QY 424 ATTGCAATGCTGCTGGGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 483
Db 427 GTGAGGATCTGGGCTGAGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGAG 486
QY 484 TTTGCTGAAAAGCCCTCTCTGTATATAGATACCATGTTCTTATGCTTCAATAGCAGT 543
Db 487 TTTGCCAGGAAGCCGTTCTGTGTATGATATGATGATGATGATGATGATGATGAT 546
QY 544 GTTTCCTCAAAATCTGAGGTAATATTTTGGCACGTGCTGACTGAGAAGTCCGTTTC 603
Db 547 CTGGCTGCTGCTTCCAGGGCAATGCTTTGCCACATCTGGCTTGGAGCTTGGCGTTC 606
QY 604 CTACAGATCCCTCCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 663
Db 607 TTGCAAAATCTTGGGAGTATGATCCGATATGAGACCGGAGGGTGGCAGCTCTTGGGA 666
QY 664 TCAAGTGTATGCTGCTACAGCAAGAAATTAATCAAGCTTGTATAGATTTTGGT 723
Db 667 TCGGATGCTACAGCTCAGCAAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 726
QY 724 CTATATTTTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 783
Db 727 CTATCTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 786
QY 784 ACATATGACAGATGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 843
Db 787 ACCTAGGCAATGACACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 846
QY 844 AAACATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 903
Db 847 AAGTACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 906
QY 904 TCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 963
Db 907 TCGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 966
QY 964 CAACACCGCCAGAAACATTTGAGAAAAGAAAGAACCCAGCTGCAACCTTATTCAGT 1023
Db 967 CAGCATCTGGGAAAACACTTTGAGAAAAGGAGGAGAACCTTGGGAGAGCTATTCAGCT 1026
QY 1024 GTTGGCGTATGTTACGAGCTGAT----- 1047
Db 1027 GCTTGGAGATTTCTATGCTACTACTCTCTCAAGCAGCAGCTGACCTCCAGCTGAGTAC 1086
QY 1048 -----GAGAAATCTGTTTCCATTTGCAACCTGGAAGCCACACTTGAAGCCTTGCACACTGC 1104
Db 1087 TACGAGCGAAGCACTACTGCTCCCATGTACAGCTCACAAACTCAAACTATGGGCGCTCC 1146
QY 1105 AGCCCTTAC-----AATCAGAAGCTAGATTTA 1132
Db 1147 AGACTCATCTCCACTCTGAAACAGCTGAGCTGCTGAGAAATCTCAAGAGCAAAATCTGGA 1206
QY 1133 AGAGAGGAGTGCAGATGCTAGCCCAAGGGCCAGAGATATTAAGAGCCGAGCAAGCCTGAG 1192
Db 1207 CTCACCTTCAGGAAGGAGCCACAGCAGAGCATCACCAAGCCCGAGGAGATGGCTGCC 1266
QY 1193 TAGGTGACGAGAGTCCCAAGCAGCATCACAGC----- 1229

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Db 1267 AAGGGAAGAGGGCTCTCCCAAGGCCACAGCGTCCGCGGCTCCCACTGGCATACAGT 1326
QY 1230 -CGAGGGAGTCCCAACAAAGTGACAGAGAGCTGGAGCTTCAAGACCGAGTTC 1287
Db 1327 CTGATATGACAGCCCGAGCAAGAGTCCCAAGAGCTTGGAGTCCGAGCGGACCA 1386
QY 1288 CGGCGCTCGCTGGGCTCCAAAGTCTCAGCCAAACCAAGATGATGCTGACACAGCC 1347
Db 1387 CGCGAGGCTTCCGATCAAGGCTGATCCGCGAGAAATTCAGAAAGCAAGCCCTC 1446
QY 1348 CTGCGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1407
Db 1447 CTTGGGAGAGACATCTTGAAGAGACAGAGCTGTAAGTCTGAGCTGATGATGATGAT 1506
QY 1408 CTACCCCACTTAAACTGATTCAGAGCTATCAAGATTAAGAAATTTATGATGCA 1467
Db 1507 CTTACCCCTGGCTCAAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1566
QY 1468 AAGCGAAGTTTAAAGAAAGTATGATGATGATGATGATGATGATGATGATGATGAT 1527
Db 1567 AAGCGAAGTTTAAAGAAAGTATGATGATGATGATGATGATGATGATGATGATGAT 1626
QY 1528 TCTGCTGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1587
Db 1627 TCGGCTGAGACACTTGTATGATGATGATGATGATGATGATGATGATGATGATGAT 1686
QY 1588 ATTCTTGGAAAAGGCAATACATCATGATTAAGAAAGCCGAGGAAAATTAACGAGAA 1647
Db 1687 ATTGTGGGGGGGGCCCAACAAATTAAGATTAAGAAAGCCGAGGAAAATTAACGAGAA 1743
QY 1648 CATGAGACACAGACATCTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1707
Db 1744 ACGGAGCTGCGCGAAGACCCCAAGATGATGATGATGATGATGATGATGATGATGAT 1803
QY 1708 CAGTCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1755
Db 1804 TTGCTCATGGAAGAAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1851

RESULT 13
AAK26588
ID AAK26588 standard; DNA; 2169 bp.
XX
AC AAK26588;
XX
DT 16-JUN-1999 (first entry)
XX
DE Nucleotide sequence of murine KCNQ2 (formerly known as (KvLRI)).
XX
KW KCNQ protein; nervous system-specific potassium channel;
KW neuronal excitability; neurotransmitter release; KCNQ modulator;
KW ataxia; myokymia; seizure; Alzheimer's disease; Parkinson's disease;
KW age-associated memory loss; learning deficiency; motor neuron disease;
KW epilepsy; stroke; ss.
XX
OS Mus sp.
XX
FH Key 1.2169 Location/Qualifiers
FT CDS /*tag= a
XX
PN W09907832-A1.
XX
PD 18-FEB-1999.
XX
XX 26-JUN-1998; 98WO-US13276.
XX
PR 12-AUG-1997; 97US-0055599.
XX
PA (BRIM ) BRISTOL-MYERS SQUIBB CO.
XX
XX Binar MA, Dworetzky S, Gribkoff VK, Levesque PC;
XX Little WA, Neubauer MG, Yang W;
PI

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QY	181	TACACGAGTACCGAGAGTGGCCGGCGCAAGTCAAGTACGGCGGATCCAGACTACTG	240
Db	223	TACACGAGTACCGAGAGTGGCCGGCGCAAGTCAAGTACGGCGGATCCAGACTACTG	282
QY	241	TACACGAGTGGAGAGAGACCCGGCGGCTGGGCTGTCATCTACACAGCTTTCGTTTTTC	300
Db	283	TACACGAGTGGAGAGAGACCCGGCGGCTGGGCGTTCATCTACACAGCTTTCGTTTTTC	342
QY	301	CTTGTCTTTGGTTCCTGATTTTGTCACTGTTTTTCTACCATCCCTGACACACAAATTC	360
Db	343	CTTGTCTTTGGTTCCTGATTTTGTCACTGTTTTTCTACCATCCCTGACACACAAATTC	402
QY	361	GCCATCAATGGCTCTTATTCCTGGAGTTCGGATGATTCGTCCTTTGGAGCTTC	420
Db	403	GCCATCAATGGCTCTTATTCCTGGAGTTCGGATGATTCGTCCTTTGGAGCTTC	462
QY	421	ATCATTCGATTCGTCTGCGGGTTCCTGTCGATATAGAGATGGCAGAGACTG	480
Db	463	ATCATTCGATTCGTCTGCGGGTTCCTGTCGATATAGAGATGGCAGAGACTG	522
QY	481	AGCTTTGCTCGAAGCCCTTC	501
Db	523	AGCTTTGCTCGAAGCCCTTC	543
RESULT 15			
AA574832			
ID	AA574832 standard; cDNA; 7413 BP.		
XX	AA574832;		
AC			
XX			
DT	13-FEB-2002 (first entry)		
XX			
DE	DNA encoding novel human diagnostic protein #10636.		
KW	Human; chromosome mapping; gene mapping; gene therapy; forensic;		
KW	food supplement; medical imaging; diagnostic; genetic disorder; ss.		
XX			
OS	Homo sapiens.		
XX			
PN	WO200175067-A2.		
PD			
XX	11-OCT-2001.		
PF	30-MAR-2001; 2001WO-US08631.		
XX			
PR	31-MAR-2000; 2000US-0540217.		
PR	23-AUG-2000; 2000US-0649167.		
XX			
PA	(HYSE-) HYSEQ INC.		
XX			
PI	Drmanac RT, Liu C, Tang YT;		
XX			
DR	WPI: 2001-639362/73.		
XX	P-PSDB; ABG10645.		
PT	New isolated polynucleotide and encoded polypeptides, useful in		
PT	diagnostics, forensics, gene mapping, identification of mutations		
PT	responsible for genetic disorders or other traits and to assess		
PT	biodiversity -		
XX			
PS	Claim 1; SEQ ID No 10636; 103pp; English.		
XX			
CC	The invention relates to isolated polynucleotide (I) and		
CC	polypeptide (II) sequences. (I) is useful as hybridisation probes,		
CC	polymerase chain reaction (PCR) primers, oligomers, and for chromosome		
CC	and gene mapping, and in recombinant production of (II). The		
CC	polynucleotides are also used in diagnostics as expressed sequence tags		
CC	for identifying expressed genes. (I) is useful in gene therapy techniques		
CC	to restore normal activity of (II) or to treat disease states involving		
CC	(II). (II) is useful for generating antibodies against it, detecting or		
CC	quantitating a polypeptide in tissue, as molecular weight markers and as		

... on the

(without alignments)
17745.835 Million cell and

scoring table: IDENTITY NIIC
.....cccaagccdaactgaataa 2667

Total number of hits containing

Minimum DB set length: 32308132

Post-processing with:
 ... ds seq length: 20000000000

Maximum Match 1008
Listing first 45

LaLaBase

1: em_estb: *
2: em_estbm: *
3: em_esth: *
4: em_esti: *
5: em_estu: *
6: em_estv: *
7: em_estp: *
8: em_hic: *
9: gb_est1: *
10: gb_est2: *
11: gb_hic: *
12: gb_est3: *
13: gb_est4: *
14: gb_est5: *
15: em_esthm: *
16: em_estom: *
17: gb_gss: *
18: em_gss_hum: *
19: em_gss_inv: *
20: em_gss_pln: *
21: em_gss_vtt: *
22: em_gss_fam: *
23: em_gss_mam: *
24: em_gss_mus: *
25: em_gss_others: *
26: em_gss_pro: *
27: em_gss_pro: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Querry	Match	Length	DB	ID	Description
	1	637.2	23.9	658	10	BE158938		BE158938 MR0-HT04
	2	553.8	20.8	734	12	BG532543		BG532543 60256210
	3	536.4	20.1	547	13	BI034993		BI034993 QV2-NN200
C	4	530.8	19.9	570	13	BI033850		BI033850 QV2-NN200
C	5	528.4	19.7	679	10	BE647997		BE647997 UY-M-BH1
	6	522	19.6	908	12	BF240146		BF240146 601905649

7	516.8	19.4	584	10	AM049888	
C	9	487.4	18.3	506	12	BF95996
	10	487	18.3	632	10	BF624101
	11	474	17.8	491	12	BF959488
C	12	454.8	15.6	435	12	BF943257
	13	415.8	15.5	469	10	BE103175
	14	403	15.1	517	12	BF954375
	15	400.8	15.0	568	14	BO339931
C	16	378.4	14.2	477	17	AZ443500
C	17	359.6	13.3	548	13	BI290441
C	18	310.8	11.7	452	12	BG732557
	19	302.2	11.3	427	12	BF523361
	20	301.4	11.3	914	12	BF312386
	21	298.8	11.2	515	12	BF962769
	22	279.8	10.5	597	9	AI589812
	23	275.8	10.3	625	10	BF666833
	24	270.2	10.1	1004	14	BO219245
	25	266.4	9.7	920	12	BF317022
	26	259.8	9.0	266	14	BO340178
	27	256.8	9.6	541	9	AI966605
	28	249.8	9.4	626	10	BF655544
C	30	242.4	9.1	771	9	AI517016
	31	241	9.0	502	9	AI018222
	32	239.4	8.6	766	11	AK020325
	33	230	8.5	282	9	AI600318
	34	227.6	8.2	469	9	AI604354
C	35	217.8	8.2	655	12	BF435555
	36	216	8.1	300	9	AI576388
	37	214.8	8.1	438	14	BO285922
	38	207.4	7.8	224	12	BF954372
	39	206.4	7.7	698	13	BM604040
	40	205.6	7.7	407	9	AI871198
C	41	202.6	7.6	648	10	AV838444
	42	198.2	7.5	622	10	BE257127
	43	196.2	7.4	555	9	AL588359
	44	192	7.2	232	12	BE860721
						AM049888 UT-M-BH1
						BF95996 OV2-NN004
						BF624101 BB624101
						BF959488 OV2-NN004
						BF9609854 BB609854
						BF943257 OV2-NN004
						BE103175 UT-R-BT1
						BF954375 OV2-NN004
						BO339931 OV2-NN004
						AZ443500 IM0238H18
						BI290441 UT-R-DKO-
						BG732557 333306 MA
						BF523361 UT-R-GO-U
						BF312386 601898926
						BF962769 OV2-NN004
						AI589812 tm741E08.x
						BE266833 601151405
						BO219245 BB666833
						BF624985 AGENCOURT
						BF317022 601903470
						BO340178 OV2-NN200
						AI966605 wt96010.x
						BF655544 BB655544
						BF945372 OV2-NN004
						AI517016 CH27636.5
						AI418222 ft74a03.x
						AI020325 Mus muscu
						AI600318 UT-R-GO-U
						AI664554 w154c06.x
						BF435555 na056f05.
						AI576388 UT-R-YO-V
						BO285922 iK23e09.x
						BF954374 OV2-NN004
						BM604040 170006877
						AI871198 w170906.x
						AV838444 AV838434
						BE257127 601108867
						AL588359
						BE860721 UT-M-A11

ALIGNMENTS

RESULT 1	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE
BE158938	BE158938	MRO-HT04	210200-001	c04	HT0404	658 bp
		BE158938				mRNA
		BE158938.1	GI:8621659			linear
		human				Homo sapiens cDNA, mRNA sequence.

ORGANISM Homo S

REFERENCE
AUTHORS
1 (bases 1 to 658)
Dias, M. A. L. (1998). *Phylogenetic relationships of the order Euteleostomi, with special reference to the suborder Euteleostomi, and the order Euteleostomi, with special reference to the suborder Euteleostomi*. *Journal of Molecular Evolution*, 47, 1-10.

TITLE Shotgun sequencing of the human transcriptome with cDNA microarrays

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 MEDLINE
 20202663
 COMMENT
 Contact: Simpson A. I.

Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, São Paulo-SP,
Brazil
Tel: +55-11-2704922
Tel: +55-11-2707001
Fax: +55-11-2707001

QY 2411 GGAGTGAGTCAGTGGCTCCAGAGCCAGCCAGATTTTACCCTCAAGTGGAGGAATCCA 2470
 |||||||
 Db 301 GGAGTGAGTCAGTGGCTCCAGAGCCAGCCAGATTTTACCCTCAAGTGGAGGAATCCA 360
 QY 2471 AATTGTTATATACGATGATGAAGAGTGGGGTCCCGAAGAGACAGACAGACACTTTTGATG 2530
 |||||||
 Db 361 AATTGTTATATACGATGATGAAGAGTGGGGTCCCGAAGAGACAGACAGACACTTTTGATG 420
 QY 2531 CCGACCGCAGCCTGCCAGGGAAGCTGCTTTGCATCAGACTCTCTAAAGACTGGAAGGT 2590
 |||||||
 Db 421 CCGACCGCAGCCTGCCAGGGAAGCTGCTTTGCATCAGACTCTCTAAAGACTGGAAGGT 480
 QY 2591 CACGATCATCTCAGAGCATTTTGTAAAGCAGAGAAAGTACAGATGCCCTCAGCTTGCCTC 2650
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 Db 481 CACGATCATCTCAGAGCATTTTGTAAAGCAGAGAAAGTACAGATGCCCTCAGCTTGCCTC 540
 QY 2651 ATGTCAACCTGAATTA 2667
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 Db 541 ATGTCAACCTGAATTA 557

RESULT 3
 LOCUS B1034993 547 bp mRNA linear EST 14-JUN-2001
 DEFINITION QV2-NN2004-120401-621-902 NN2004 Homo sapiens cDNA, mRNA sequence.
 ACCESSION B1034993
 VERSION B1034993.1 GI:14441619
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 547)
 Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
 Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
 Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,
 Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
 M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
 Simpson,A.J.
 Shotgun sequencing of the human transcriptome with ORF expressed
 sequence tags

TITLE Shotgun sequencing of the human transcriptome with ORF expressed
 sequence tags
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 MEDLINE 20202663
 COMMENT Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome
 Project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/scripts/gethtml2.pl?l1-QV2&l2-QV2-NN2004-
 120401-621-902&l3-2001-04-12&l4-1)
 Seq primer: puc 18 forward
 High quality sequence stop: 543.

FEATURES
 source
 1..547
 Location/Qualifiers
 1..547
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="NN2004"
 /dev_stage="Adult"
 /note="Organ: nervous normal; Vector: puc18; Site_1: SmaI;
 Site_2: SmaI; A mini-library was made by cloning products
 derived from ORESTES PCR (U.S. Letters Patent application
 No. 196,716 - Ludwig Institute for Cancer Research)
 profiles into the pUC 18 vector. Reverse transcription of
 tissue mRNA and cDNA amplification were performed under
 low stringency conditions."
 low stringency conditions."

BASE COUNT
 ORIGIN

175 a 127 c 116 g 129 t

Query Match 20.1% Score 536.4; DB 13; Length 547;
 Best Local Similarity 98.9%; Pred. No. 4.5e-121;
 Matches 540; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1268 TCAACGACCGAACCCGCTTCCGGCCCTCGTCGCGCTCAAAAAGTTCTCAGCCAAAACCG 1327
 |||||||
 Db 1 TCAACGACCGAACCCGCTTCCGGCCCTCGTCGCGCTCAAAAAGTTCTCAGCCAAAACCG 60
 QY 1328 TGATATGATGCTGACACAGACCTTGGACATGATGATATATGATGATGATGATGATG 1387
 |||||||
 Db 61 TGATATGATGCTGACACAGACCTTGGACATGATGATATGATGATGATGATGATGATGATG 120
 QY 1388 GTGATGATGCTGACAGAGACCTTCCACCTGATGATGATGATGATGATGATGATGATG 1447
 |||||||
 Db 121 GTGATGATGCTGACAGAGACCTTCCACCTGATGATGATGATGATGATGATGATGATGATG 180
 QY 1448 TTATGAATTTTCATGTTGCAAAAGGAAAGTTAAAGAAAGCTTACGCTCATATGATGTA 1507
 |||||||
 Db 181 TTATGAATTTTCATGTTGCAAAAGGAAAGTTAAAGAAAGCTTACGCTCATATGATGTA 240
 QY 1508 AAGATGTCATTTGAACAATATTTCTGCTGTCATCTGACATGTTGTGATGAATTAAGACC 1567
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 Db 241 AAGATGTCATTTGAACAATATTTCTGCTGTCATCTGACATGTTGTGATGAATTAAGACC 300
 QY 1568 TTCAACACGCTGTGATCAAAATTTCTTGGAAAGGCAAAATCAGATCAGATTAAGAGACC 1627
 |||||||
 Db 301 TTCAACACGCTGTGATCAAAATTTCTTGGAAAGGCAAAATCAGATCAGATTAAGAGACC 360
 QY 1628 GAGAGAAATTAACAGCAGAACATGAGACACAGACATCTCAGATGCTCGCTGCGTGG 1687
 |||||||
 Db 361 GAGAGAAATTAACAGCAGAACATGAGACACAGACATCTCAGATGCTCGCTGCGTGG 420
 QY 1688 TCAAGGTTGAAAAACAGTCCAGTCCATAGAGTCCAAAGCTGACTGCTACTAGACATCT 1747
 |||||||
 Db 421 TCAAGGTTGAAAAACAGTCCAGTCCATAGAGTCCAAAGCTGACTGCTACTAGACATCT 480
 QY 1748 ATCAACAGTCTCTCGGAAAGGCTCTGCTCAGCCCTGCTTGGCTTCATTTCAGATCC 1807
 |||||||
 Db 481 ATCAACAGTCTCTCGGAAAGGCTCTGCTCAGCCCTGCTTGGCTTCATTTCAGATCC 540
 QY 1808 CACCTT 1813
 |||||||
 Db 541 CACCTT 546

RESULT 4
 LOCUS B1033850 570 bp mRNA linear EST 14-JUN-2001
 DEFINITION QV2-NN2003-080301-615-c09 NN2003 Homo sapiens cDNA, mRNA sequence.
 ACCESSION B1033850
 VERSION B1033850.1 GI:14440476
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 570)
 Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
 Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
 Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,
 Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
 M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
 Simpson,A.J.
 Shotgun sequencing of the human transcriptome with ORF expressed
 sequence tags

TITLE Shotgun sequencing of the human transcriptome with ORF expressed
 sequence tags
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 MEDLINE 20202663
 COMMENT Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil
 Tel: +55-11-2704922

BASE COUNT
 ORIGIN

175 a 127 c 116 g 129 t

JOURNAL
MEDLINE
COMMENT

Genome Res. 6 (9), 791-806 (1996)

Contact: Chin, H

National Institute of Mental Health

6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD

20892-9643, USA

Tel: 301 443 1706

Fax: 301 443 9890

Email: mestr@mail.nih.gov

Oligo-dT track not found, Not I site shown in beginning of sequence is likely internal to the message. cDNA Library Preparation: M.B. Soares Lab Clone distribution: NIH BMAP cDNA clones will be made available by the means that is soon to be determined. When NIH determines the means for distribution of the BMAP cDNA clones, this record will be updated accordingly when that means is determined. The following repetitive elements were found in this cDNA sequence: 37-71, >CC-richlow-complexity
Seq primer: M13 Forward
POLYA-No.

FEATURES
source

Location/Qualifiers

1..584

/organism="Mus musculus"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="U1-M-BH1-amr-g-09-0-U1"

/dev_stage="27-32 days"

/lab_host="DH10B (Life Technologies)"

/note="Vector: pTZ19-pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; The

NIH-BMAP_M_S2 library is a subtracted library derived from

NIH-BMAP_M_S1, which in turn is a subtracted library derived from a mixture of normalized libraries from ten

regions of the mouse brain (cerebellum, brain stems, olfactory bulbs, hypothalamus, cortex, amygdala, basal

ganglia, pineal gland, striatum, hippocampus). The driver

used for subtraction consisted of a pool of 5,000 clones from the NIH-BMAP_M_S1 library and a pool of 2,000 clones

obtained from non-normalized and normalized mouse brain

spinal cord libraries.

TAG_LIB=NIH_BMAP_M_S2

TAG_TISSUE=corpus-striatum

TAG_SEQ=ACGGC

BASE COUNT 107 a 151 c 174 g 152 t

ORIGIN

Query Match 19.4%; Score 516.8; DB 10; Length 584;

Best Local Similarity 92.8%; Pred. No. 3.1e-116;

Matches 542; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

47 CAGCGCCGAGGGGCGGCGCTGCTACTGCTGGGCAACCGCGCGGCGCGCTTGTGGCG 106

1 CGGCGCGGAGGGGCGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 60

107 GCGGCGGTGGCTGAGGAGAGCGCGCGGGGCAAGAGAGGGGCGCGGATGAGCTGTGG 166

61 GCGGCGGGGCTTGAAGAGAGAGCGCGCGGGGCAAGAGAGGGGCGCGGATGAGCTGTGG 120

167 GGAAGCCGCTCTCTTACAGAGTAGCCAGAGCTGCGCGGCGCAAGCTCAAGTACCGGGG 226

121 GGAAGCCGCTCTCTTACAGAGTAGCCAGAGCTGCGCGGCGCAAGCTCAAGTACCGGGG 180

227 TGCAAGACTACTGTAACAAGCTGCTGAGAGAGCGCGCGGGGCTTGTGGCGTATTCACAG 286

181 TGCAAGACTACTGTAACAAGCTGCTGAGAGAGCGCGCGGGGCTTGTGGCGTATTCACAG 240

287 CTTCGTTTTCTCTCTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 346

241 CGTTGTTTTCTCTCTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 300

347 AGCACAATAATGGCTCAAGTGGCTCTTGATCTGAGTTCGATGATGATGATGATGATG 406

301 AGCATACAAAATGGCTCAAGTGGCTCTTGATCTGAGTTCGATGATGATGATGATGATG 360

QY 407 TTGGTTGAGATTCATCATTCGAATCTGCTGCCGGTTGCTGTTGTCGATATAGAGAT 466
Db 361 TTGGTTGAGATTCATCATTCGAATCTGCTGCCGGTTGCTGTTGTCGATATAGAGAT 420
QY 467 GCGAAGAGAGACTGAGTTGCTGGAAGAGCCCTTCTGTTATGATACCATTTGTTCTTA 526
Db 421 GCGAAGAGAGACTGAGTTGCTGGAAGAGCCCTTCTGTTATGATACCATTTGTTCTTA 480
QY 527 TCGTTTCAATAGCAGTTGTTCTTCCAAAACACTCAGGTAATATTTTCCACGCTTCGAC 586
Db 481 TCGTTTCAATAGCAGTTGTTCTTCCAAAACACTCAGGTAATATTTTCCACGCTTCGAC 540
QY 587 TCAGAGTCTCCGTTTCTCTACAGATCCCGCATGAGTGGCATG 630
Db 541 TCAGAGTCTCCGTTTCTCTACAGATCCCGCATGAGTGGCATG 584

RESULT 8
LOCUS BF959996/c 506 bp mRNA linear EST 22-JAN-2001
DEFINITION OV2-NN0045-051200-526-g09 NN0045 Homo sapiens cDNA, mRNA sequence.
ACCESSION BF959996
VERSION BF959996.1 GI:12377271
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 506)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Goldman, G.H., Cavvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H.,
Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare,
M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?cl=GV2&t2=GV2-NN0045-
051200-526-g09&t3=2000-12-05&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 506.

TITLE
JOURNAL
MEDLINE
COMMENT

FEATURES
source

Location/Qualifiers

1..506

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone_lib="NN0045"

/dev_stage="Adult"

/note="Organ: nervous normal; Vector: puc18. Site 1: SmaI;

Site 2: SmaI. A mini-library was made by cloning products

derived from ORSTS PCR (U.S. Letters Patent application

No. 196,716 - Ludwig Institute for Cancer Research)

profiles into the puc 18 vector. Reverse transcription of

tissue mRNA and cDNA amplification were performed under

low stringency conditions "

BASE COUNT 125 a 108 c 104 g 168 t 1 others

ORIGIN

Query Match 18.3%; Score 487.4; DB 12; Length 506;

Best Local Similarity 97.6%; Pred. No. 5.1e-109;

Matches 494; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

[illegible]

COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP.

Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
 (<http://www.ludwig.org.br/scripts/gethtml2.pl?pl=QV2&QV2-QV2-NN0045-041000-403-h12&QV2-2000-10-04&QV2-1>)
 Seq primer: puc 18 forward
 High quality sequence stop: 15
 Location/Qualifiers
 1. 433
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_1ib="NN0045"
 /dev_stage="Adult"
 /note="Organ: nervous_normal; Vector: puc18; Site_1: Sma1; Site_2: Sma1; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196/716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

BASE COUNT 110 a 94 c 89 g 142 t
 ORIGIN

Query Match 15.6%; Score 415.8; DB 12; Length 435;
 Best Local Similarity 99.5%; Pred. No. 2.1e-91;
 Matches 417; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1428 TGCATTCGAGCATCAGATTTGAATTTTCATGTTGCAGAAACGGAAGTTTAAAGAAC 1487
 DB 435 TGTCAATTCGAGCATCAGATTTGAATTTTCATGTTGCAGAAACGGAAGTTTAAAGAAC 376
 OY 1488 GTTACGTCATATGATGTAAAGATGTCATTTGTAACATATTTCTGTCATCTGGACAT 1547
 DB 375 ATTACGTCATATGATGTAAAGATGTCATTTGTAACATATTTCTGTCATCTGGACAT 316
 OY 1548 GTTGTGTAAATTTAAAGCCTTCAACACGCTGTTGATCAAAATCTTGGAAAAGGCAAAAT 1607
 DB 315 GTTGTGTAAATTTAAAGCCTTCAACACGCTGTTGATCAAAATCTTGGAAAAGGCAAAAT 256
 OY 1608 CACATCAGATTAAGAGAGCGGAGAGAAATTAACAGCAAGATGAGACCCAGACGATCT 1667
 DB 255 CACATCAGATTAAGAGAGCGGAGAGAAATTAACAGCAAGATGAGACCCAGACGATCT 196
 OY 1668 CAGTATGCTGGTGGGTGGTCAAGGTTGAAAAACAGTACATCCATAGTCCAAAGCT 1727
 DB 195 CAGTATGCTGGTGGGTGGTCAAGGTTGAAAAACAGTACATCCATAGTCCAAAGCT 136
 OY 1728 GAGCTGCTAGTACATCTATCAACAGGTCCTTGGAAAAGGCTTGCCTCAGCCCTCGC 1787
 DB 135 GAGCTGCTAGTACATCTATCAACAGGTCCTTGGAAAAGGCTTGCCTCAGCCCTCGC 76
 OY 1788 TTGGGCTTCATTCAGATCCCACTTTTGAATGTGAAGACATCGACTATCAAGGCC 1846
 DB 75 TTGGGCTTCATTCAGATCCCACTTTTGAATGTGAAGACATCGACTATCAAGGCC 17

RESULT 13
 BE103175 469 bp mRNA linear EST 13-JUN-2000
 LOCUS BE103175
 DEFINITION UI-R-BT1-agx-h-11-0-UI.s1 UI-R-BT1 Rattus norvegicus cDNA clone
 ACCESSION BE103175
 VERSION BE103175.1 GI:8495314
 KEYWORDS EST.
 SOURCE Norway rat.
 ORGANISM Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.

REFERENCE 1 (bases 1 to 469)
 AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
 TITLE Normalization and subtraction: two approaches to facilitate gene discovery
 JOURNAL Genome Res. 6 (9), 791-806 (1996)
 MEDLINE 97044477
 COMMENT Contact: Soares, MB
 Program for Rat Gene Discovery and Mapping
 University of Iowa
 451 Eckstein Medical Research Building Iowa City, IA 52242, USA
 Tel: 319 335 8250
 Fax: 319 335 9565
 Email: msoares@blue.weeg.uiowa.edu
 Oligo-dT track not found. Not 1 site shown in beginning of sequence
 is likely internal to the message. cDNA library preparation: M.B.
 Soares Lab Clone distribution: clones will be available through
 Research Genetics (www.resgen.com) The following repetitive
 elements were found in this cDNA sequence: 1-71,
 >GC-rich#Low-complexity
 Seq primer: M13 Forward
 POLYA-No.

FEATURES
 source Location/Qualifiers
 1. 469
 /organism="Rattus norvegicus"
 /strain="Sprague-Dawley"
 /db_xref="taxon:10116"
 /clone_1ib="UI-R-BT1-agx-h-11-0-UI"
 /dev_stage="Adult"
 /lab_host="DH10B (Life Technologies)"
 /note="Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; The library UI-R-BT1 is a subtracted library derived from a mixture of the following tissues: hippocampus, thalamus, mid-brain, medulla, corpus striatum, cerebral cortex and testis. For a detailed description of the library from which this clone was derived, please visit our web site at ratest.eng.uiowa.edu. The subtraction has been previously described in (Bonaldo, Lennon and Soares, Genome Research 6:791-806, 1996)
 TAG-SEQ=None found"

BASE COUNT 79 a 120 c 152 g 118 t
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Query Match 15.5%; Score 414.6; DB 10; Length 469;
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 DB 121 GGAAGCGGCTCTTTAAGCAGTACAGAGCTGCGGCGCAAGCTCAAGTACCGCGGG 180
 OY 227 TGCAGACTACTGTACAGAGCTGTGAGAGAGCCCGGCGTGGGCTTCAATCAACAGC 286
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OY 467 GCCAAGGAGCTGAGGTTTGTCTGGAAGCCCTTCTGTTAGATAC 515
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DEFINITION BF954375
ACCESSION BF954375
VERSION BF954375.1 GI:12371650
KEYWORDS EST.
SOURCE human.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Nagel,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,
Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QV2&tl2=QV2-NN0045-
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Site:2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
BASE COUNT 169 a 106 c 123 g 119 t
ORIGIN
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Matches 479; Conservative 0; Mismatches 30; Indels 8; Gaps 5;

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OY 1500 TCAATGTAAGAAATGTCATGTAAGCAATATTCGTCGTCATCTGACATGTTGTAGAAAT 1559
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ACCESSION BO339931
VERSION BO339931.1 GI:21000109
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SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagel,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,
Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QV2&tl2=QV2-NN0045-
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Location/Qualifiers
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/clone_lib="NN0045"
/dev_stage="Adult"
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Site:2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)

Profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions.
BASE COUNT 176 a 121 c 128 g 143 t
ORIGIN

Query Match 15.0%; Score 400.8; DB 14; Length 568;
Best Local Similarity 86.2%; Pred. No. 1.1e-87;
Matches 481; Conservative 0; Mismatches 67; Indels 10; Gaps 3;

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Job time : 2452 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 11, 2003, 15:52:07 : Search time 74 Seconds

(without alignments)
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Title: US-09-810-796-3

Perfect score: 2667

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Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 441362 seqs, 15333831 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	475.6	17.8	2169	4	US-09-105-058C-22
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4	427.2	16.0	2565	4	US-09-105-058C-26
5	427.2	16.0	2914	4	US-09-177-650-6
6	426.8	16.0	2814	4	US-09-177-650-90
7	425	15.9	3287	4	US-09-105-058C-19
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34	60.8	2.3	859	4	US-09-177-650-117	Sequence 117, App
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38	53.6	2.0	215	4	US-09-177-650-103	Sequence 103, App
39	52.8	2.0	238	4	US-09-177-650-105	Sequence 105, App
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41	45	1.7	7218	1	US-08-232-463-14	Sequence 14, App
42	43.2	1.6	7218	1	US-08-232-463-14	Sequence 14, App
43	42.8	1.6	226	4	US-09-105-058C-9	Sequence 9, App
44	42	1.6	508	1	US-08-318-193-69	Sequence 69, App
45	41.8	1.6	3424	4	US-09-336-643A-9	Sequence 9, App

ALIGNMENTS

RESULT 1	
US-09-177-650-88	
Sequence 88, Application US/09177650	
Patent No. 6413719	
GENERAL INFORMATION:	
APPLICANT: Leppert, Mark F.	
APPLICANT: Singh, Nanda	
TITLE OF INVENTION: Charlier, Carole	
TITLE OF INVENTION: MUTATED IN BENIGN FAMILIAL NEONATAL CONVULSIONS (BFNC)	
FILE REFERENCE: 2323-134	
CURRENT APPLICATION NUMBER: US/09/177,650	
EARLIER FILING DATE: 1998-10-23	
EARLIER APPLICATION NUMBER: 60/063,147	
NUMBER OF SEQ ID NOS: 129	
SOFTWARE: PatentIn Ver. 2.0	
SEQ ID NO 88	
LENGTH: 2273	
TYPE: DNA	
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FEATURE:	
NAME/KEY: CDS	
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US-09-177-650-88	
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Best Local Similarity 57.08; Pred. No. 5,7e-136;	
Matches 1020; Conservative 2; Mismatches 667; Indels 99; Gaps 4;	
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; Sequence 22, Application US/09105058C
; Patent No. 6403360
; INFORMATION:

APPLICANT: Blanaid

APPLICANT: Gribkov

APPLICANT: Little

APPLICANT: Yang, Y

FILE OF INVENTION;
THE PATENT OFFICE;
3

CURRENT FILLING DAY

PRIOR FILING DATE:

SEC ID NO 22

LENGTH. 2100
TYPE. DNA

US-09-105-058C-22

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 Oy GTCTTTGGTCTGATTTGTCAGTGTCTTTTCTACCATCTTGAGACACAAATTTGCC 353
 Db 547 CTGGCTGCTGCTTCCAGGCAATGCTTTGCTCATCTGCTGCTGCTGCTGCTGCTGCT 606
 Oy GTCTTTGGTCTGATTTGTCAGTGTCTTTTCTACCATCTTGAGACACAAATTTGCC 353
 Db 604 CTACAGATCTCCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 663
 Oy GTCTTTGGTCTGATTTGTCAGTGTCTTTTCTACCATCTTGAGACACAAATTTGCC 353
 Db 607 TTTGCAATCTTCCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 666
 Oy GTCTTTGGTCTGATTTGTCAGTGTCTTTTCTACCATCTTGAGACACAAATTTGCC 353
 Db 664 TCAGTGTCTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 723
 Oy GTCTTTGGTCTGATTTGTCAGTGTCTTTTCTACCATCTTGAGACACAAATTTGCC 353
 Db 667 TCGTAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 726
 Oy GTCTTTGGTCTGATTTGTCAGTGTCTTTTCTACCATCTTGAGACACAAATTTGCC 353
 Db 724 CTATATTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 783
 Oy GTCTTTGGTCTGATTTGTCAGTGTCTTTTCTACCATCTTGAGACACAAATTTGCC 353
 Db 727 CTATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 786
 Oy GTCTTTGGTCTGATTTGTCAGTGTCTTTTCTACCATCTTGAGACACAAATTTGCC 353
 Db 784 ACATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 843
 Oy GTCTTTGGTCTGATTTGTCAGTGTCTTTTCTACCATCTTGAGACACAAATTTGCC 353
 Db 787 ACCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 846
 Oy GTCTTTGGTCTGATTTGTCAGTGTCTTTTCTACCATCTTGAGACACAAATTTGCC 353
 Db 844 AAAACTCCCTTAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 903
 Oy GTCTTTGGTCTGATTTGTCAGTGTCTTTTCTACCATCTTGAGACACAAATTTGCC 353
 Db 847 AAGTACCTCCAGACCTGGAACGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 906
 Oy GTCTTTGGTCTGATTTGTCAGTGTCTTTTCTACCATCTTGAGACACAAATTTGCC 353
 Db 904 TCTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 963
 Oy GTCTTTGGTCTGATTTGTCAGTGTCTTTTCTACCATCTTGAGACACAAATTTGCC 353
 Db 907 TCGTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 966
 Oy GTCTTTGGTCTGATTTGTCAGTGTCTTTTCTACCATCTTGAGACACAAATTTGCC 353
 Db 964 CAACACCGCCAGAAACATTTGAGAAAGAAAGAACCCAGCTGCCAACCCTATTCAGTCT 1023
 Oy GTCTTTGGTCTGATTTGTCAGTGTCTTTTCTACCATCTTGAGACACAAATTTGCC 353
 Db 967 CAGCATCCGCAAAACACTTTGAGAAACGCGGAGAACCTCGGCGAGGCTGATCCAGTCT 1026
 Oy GTCTTTGGTCTGATTTGTCAGTGTCTTTTCTACCATCTTGAGACACAAATTTGCC 353
 Db 1024 GTTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1083
 Oy GTCTTTGGTCTGATTTGTCAGTGTCTTTTCTACCATCTTGAGACACAAATTTGCC 353
 Db 1027 GCCTGAGATTTCTATGCTTAACTCTCACGCAACCCAGCTGCACTCCACGTTGAGTAC 1086
 Oy GTCTTTGGTCTGATTTGTCAGTGTCTTTTCTACCATCTTGAGACACAAATTTGCC 353
 Db 1084 T----- 1084
 Oy GTCTTTGGTCTGATTTGTCAGTGTCTTTTCTACCATCTTGAGACACAAATTTGCC 353
 Db 1087 TAGAGCGGACAGTCACTGCCCCATGATACAGACATCCACCTTGAGACAGCTGAG 1146
 Oy GTCTTTGGTCTGATTTGTCAGTGTCTTTTCTACCATCTTGAGACACAAATTTGCC 353
 Db 1085 -----TGAAGGCTTGACACCTGCTC 1104
 Oy GTCTTTGGTCTGATTTGTCAGTGTCTTTTCTACCATCTTGAGACACAAATTTGCC 353
 Db 1147 CTGCTGAGATCTCAAGAGCAATCTGAGCTCACCTTCAGAGAGGAGCCACAGCCAGAG 1206
 Oy GTCTTTGGTCTGATTTGTCAGTGTCTTTTCTACCATCTTGAGACACAAATTTGCC 353
 Db 1105 AGCCCTCAATCCAGAGCTAAGTTTAAAGAGGAG--TGGGATGAGCTTGAAGCCAG 1161
 Oy GTCTTTGGTCTGATTTGTCAGTGTCTTTTCTACCATCTTGAGACACAAATTTGCC 353
 Db 1207 CCATCACCAGTCAAGAGCTGATTTGAAGATGCTGCTTCTGCAAGCCCGGAGGATG 1266
 Oy GTCTTTGGTCTGATTTGTCAGTGTCTTTTCTACCATCTTGAGACACAAATTTGCC 353
 Db 1162 GCGCAGAGTATTAAGAGCCGCAAGCTCAGTATGATGACAGAGGTTCCCAAGCACCGAC 1221
 Oy GTCTTTGGTCTGATTTGTCAGTGTCTTTTCTACCATCTTGAGACACAAATTTGCC 353
 Db 1267 GCTCCCAAGGAAAGGAGGCTTCCCGAGGCGCAAGAGGCTGCGGCGGCTCCCGCAGTGGGAT 1326
 Oy GTCTTTGGTCTGATTTGTCAGTGTCTTTTCTACCATCTTGAGACACAAATTTGCC 353
 Db 1222 ATCAGACCGGAGGAGGCTCCACCAAGTGCAGAGAGGCTGAGAGTTCACAGCAGCAAC 1281
 Oy GTCTTTGGTCTGATTTGTCAGTGTCTTTTCTACCATCTTGAGACACAAATTTGCC 353
 Db 1327 CAGAGTCTTGTATGACAGCGCAGAGGCTGCCAAGAGCTTGTGTACCCAGC 1386

Oy 1282 CGCTTCGGGCGCTCGCTGCGCTCAAAAGTTCTCAGCCAAAACAGATGATGCTGAC 1341
 Db 1387 CGCAGACCGCAGGCTTTCGATCAAGGCTGCTGATCCCGCAGAAATTCAGACAGAAC 1446
 Oy 1342 ACAGCCCTTGGCAGCTGATGATGATATGATGATGATGATGATGATGATGATGATGAT 1401
 Db 1447 C---TCCCTGGGAGAGCATGCTGATGAGGACCAACAGAGCTGTAAGTGGAGTTGTGACT 1503
 Oy 1402 GAAGACCTCACCCACCACTTAAACCTGATGATGATGATGATGATGATGATGATGAT 1461
 Db 1504 GAAGATCTTACCCCTGCGCTCAAAAGTATGATGATGATGATGATGATGATGATGAT 1563
 Oy 1462 GTTGCAGAAACGAGTTTAAAGAAAGTATGATGATGATGATGATGATGATGATGAT 1521
 Db 1564 GTATCTAAGCCAGAAATTAAGAGAGTCTGCGCCCATATGATGATGATGATGATGAT 1623
 Oy 1522 CAATATCTGCTGCTGATCTGATGATGATGATGATGATGATGATGATGATGATGAT 1581
 Db 1624 CAGTACTCGGCTGACACTTGTGATGATGATGATGATGATGATGATGATGATGATGAT 1683
 Oy 1582 GATCAATTTCTTGAAGAAAGGCAATTCATCAGATTAAGAAAGCCGAGAAATTAACA 1641
 Db 1684 GACCGATTTGCGGCGGCGCCCAACAAATTAAGATTAAGA--TGCACAAAGGCCCA 1740
 Oy 1642 GCAGAAATGAGACCAACAGCATCTCAGTATGCTGCTGCTGCTGCTGCTGCTGCTGCT 1701
 Db 1741 GCGGAAAGGAGAGCTCCGCAAGACCCACATGATGATGAGAGGCTTGGAAAGGTGAGAA 1800
 Oy 1702 CAGTACAGCTCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1755
 Db 1801 CAGTCTGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1854

RESULT 3
 US-09-105-058C-1
 : Sequence 1, Application US/09105058C
 : Patent No. 6403360
 : GENERAL INFORMATION:
 : APPLICANT: Blonar, Michael A.
 : APPLICANT: Dworetzky, Steven
 : APPLICANT: Grikoff, Valentin K.
 : APPLICANT: Levesque, Paul C.
 : APPLICANT: Little, Wayne A.
 : APPLICANT: Neuberger, Michael G.
 : APPLICANT: Yang, Wen-Pin
 : TITLE OF INVENTION: KCON POTASSIUM CHANNELS AND METHODS OF MODULATING SAME
 : FILE REFERENCE: 3053-4052
 : CURRENT APPLICATION NUMBER: US/09/105, 058C
 : PRIOR FILING DATE: 1998-06-26
 : PRIOR APPLICATION NUMBER: US 60/055, 599
 : PRIOR FILING DATE: 1997-08-12
 : NUMBER OF SEQ ID NOS: 28
 : SOFTWARE: Patent Ver. 2.1
 : SEQ ID NO 1
 : LENGTH: 896
 : TYPE: DNA
 : ORGANISM: Artificial Sequence
 : FEATURE:
 : OTHER INFORMATION: Description of Artificial Sequence:Consensus
 : OTHER INFORMATION: nucleotide sequence as shown in fig. 16A-16D
 : OTHER INFORMATION: w=a or t; h=a, c, or g; b=g, t, or c; v=g, c, or a
 : US-09-105-058C-1

Query Match 17.5%; Score 465.4; DB 4; Length 896;
 Best Local Similarity 53.7%; Pred. No. 4e-129;
 Matches 460; Conservative 231; Mismatches 162; Indels 4; Gaps 2;
 Oy 190 AGCCAGAGTCCGCGCAACGTAAGTACCGGCGGCTGCGAGTACTCTGACAGCTG 249
 Db 13 RSMRSCMSYSAAGMMAAGCCGCMWSTACGSMRSMSTSCARAMTTTMTCTACRAGYS 72


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OY 874 CTTTCTGAGGCTTTGACACCTCTTGATTTCTTTTGGACCTTCCTCGCGGACCTCT 933
    || || || || || || || || || || || || || || || || || || || ||
Db 940 ATGCGCGGACCTTTCTCTTAATGCGCTCTCTTTTGGCCCTTCAGCGGACCTCTG 999
OY 934 GGCCTAGCTTTTGCATTTAAAGTACAAACACACCCGCAACAACTTTTGAAGAA 993
    || || || || || || || || || || || || || || || || || || || ||
Db 1000 GGGTCGGGCTGGCCCTTAAGGTGAGAGACACACCGCTCAAGACACTTTGAGAAAG 1059
OY 994 AGGAACCCAGTCCACACCTCTATCTGTGTGTTGGCGTATTAGCAGCTATGAGAA 1053
    || || || || || || || || || || || || || || || || || || || ||
Db 1060 AGGAAGCCAGCTCTGAGCTATTCAGGCTGCTGAGTATTTGCTACCAACCCCAAC 1119
OY 1054 TCTGTTTTCATG-----CAACCTGAGAGCCCACTTGAAGGCTTGGACACCTGC 1104
    || || || || || || || || || || || || || || || || || || || ||
Db 1120 AGGATTGACCTGTGGCGCATGAGATTTTATGATCAGTGTCTCTTTCTCTTCTTC 1179
OY 1105 AGCCCTACCAATCAGAACTAAGTTTAAAGAGCGAGTGGCATGGCTAGCCGAGGGC 1164
    || || || || || || || || || || || || || || || || || || || ||
Db 1180 AGGAAGAAGACAGCTGAGAGAGATCAGCAACAAAGCTGGTCTCTTGGATCGGGTTGCG 1239
OY 1165 CAGATATTAAAGCCGACAGACGCTCAGTAGAGAGAGAGGCTCCCAAGCAGCAGATC 1224
    || || || || || || || || || || || || || || || || || || || ||
Db 1240 CTTTCTTAATCTCTGTGTAGCAATTAAGAAAGCTATTACCTCTGANTGATGAT 1299
OY 1225 ACAGCCGAGGCGAGTCCACCAAGTGCAGAGAGCTGAGCTTCAACAGCAGCCGCG 1284
    || || || || || || || || || || || || || || || || || || || ||
Db 1300 GCCATAGAAAGAAAGTCTCTTAAGAAACCAAGCTGTGGCTTAAACATTAAGAGCGT 1359
OY 1285 TTCGCGGCTCTGCGGCTTCAAAAGTTCTCAGCCAAACAGTATGATAGTGTGAGACA 1344
    || || || || || || || || || || || || || || || || || || || ||
Db 1360 TTCGCGAGGCTCTTCCATGAAGAGCTTCTTGGCAGAGTCTTGAAGATGCCGGG 1419
OY 1345 GCGCTGGCAGTGTATGATATGATGATGATGATGATGATGATGATGATGATGATG 1404
    || || || || || || || || || || || || || || || || || || || ||
Db 1420 ACAGGTACCCCATGCG-----GGAAGACAGAGGCGTATGAGATGACTTCCCATCGAA 1473
OY 1405 GACCTCAGCCACACCTTAAGTATGATGATGATGATGATGATGATGATGATGATG 1464
    || || || || || || || || || || || || || || || || || || || ||
Db 1474 GACATGATGCCACCTCGAAGGCGCGCATCGACCGCTCAAAATTTCAATTCCTGCTC 1533
OY 1465 GCAAAACCGAAGTTAAGGAACGTTACGATATGATGATGATGATGATGATGATG 1524
    || || || || || || || || || || || || || || || || || || || ||
Db 1534 TATTAATAAAATTCAGAGACTTTTGAGGCTTACGATGGAAGATGTGATTGAGAC 1593
OY 1525 TATCTGCTGCTCATCTGACATGTTGTGATGATTAAGAGCTTCAAGACAGCTGTGAT 1584
    || || || || || || || || || || || || || || || || || || || ||
Db 1594 TATCTGCGGCGCATCTGACATGCTTCCAGGATTAAGTACCTTCAGACGAGAAATGAT 1653
OY 1585 CAATTTCT 1592
    || || || || || || || || || || || || || || || || || || || ||
Db 1654 ATGATTTT 1661
    || || || || || || || || || || || || || || || || || || || ||

RESULT 5
US-09-177-650-6
; Sequence 6, Application US/09177650
; Patent No. 6413719
; GENERAL INFORMATION:
; APPLICANT: Leppert, Mark F.
; APPLICANT: Singh, Nanda
; APPLICANT: Charlier, Carole
; TITLE OF INVENTION: KCMQ2 AND KCMQ3 - POTASSIUM CHANNEL GENES WHICH ARE
; TITLE OF INVENTION: MUTATED IN BENIGN FAMILIAL CONVULSIONS (BFNC)
; TITLE OF INVENTION: AND OTHER EPILEPSIES
; FILE REFERENCE: 2323-134
; CURRENT APPLICATION NUMBER: US/09/177,650
; CURRENT FILING DATE: 1998-10-23
; EARLIER APPLICATION NUMBER: 60/063,147
; EARLIER FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 6

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; LENGTH: 2914
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (19)..(2634)
; FEATURE:
; NAME/KEY: allele
; LOCATION: (840)
; OTHER INFORMATION: The polymorphism of a T to a C at this position
; OTHER INFORMATION: has appeared in one individual.
; FEATURE:
; NAME/KEY: mutation
; LOCATION: (947)
; OTHER INFORMATION: The missense mutation from a G to a T occurs at
; OTHER INFORMATION: this position in a BFNC family.
; FEATURE:
; NAME/KEY: allele
; LOCATION: (678)
; OTHER INFORMATION: This position is polymorphic for C or T.
; FEATURE:
; NAME/KEY: allele
; LOCATION: (750)
; OTHER INFORMATION: This position is polymorphic for T or C.
; FEATURE:
; NAME/KEY: allele
; LOCATION: (1089)
; OTHER INFORMATION: This position is polymorphic for G or C.
; FEATURE:
; NAME/KEY: allele
; LOCATION: (2598)
; OTHER INFORMATION: This position is polymorphic for T or C.
; OTHER INFORMATION: This position is polymorphic for T or C.
US-09-177-650-6

Query Match 16.0%; Score 427.2; DB 4; Length 2914;
Best Local Similarity 56.7%; Pred. No. 2.4e-117;
Matches 923; Conservative 0; Mismatches 648; Indels 57; Gaps 5;

OY 13 GAGTCGGGCGGGGCGAGGCTGCTGTAATCGGAGCGCCGCAAGGGGAGAGCGCTGTA 72
    || || || || || || || || || || || || || || || || || || || ||
Db 115 GCGGCGGCGGCGCGAGAGAGAGCGGAAGTGGGCTGGCCCGCGGAGCTGAGCA 174
OY 73 CTGCTGGGCACCCGGGGCGGCGACCTGTGGGCGGCGGCTGAGGAGAGCGCG 132
    || || || || || || || || || || || || || || || || || || || ||
Db 175 GTACCTTGGCGCTGGGCGCGGAGCCGAGCCGCAAGAGCGGAGCCCTGAGGAGCGCG 234
OY 133 CGGGCAAGCAGAGGGGCGCGGATGAGCTGTGGGAGAGCCGCTCTTACACAGATAC 192
    || || || || || || || || || || || || || || || || || || || ||
Db 235 GCGCGGAGAGAGGGGAGCGGAGGAGACCCGAGGAGCATGGGCTCTGCGCAAGACCGG 294
OY 193 CAGAGCTGCC-----GCGCAACGTCAGATACCGGCGGGTGCAGAACTACCTGTAC 243
    || || || || || || || || || || || || || || || || || || || ||
Db 295 CTGAGCGCGCCAGTCAAGAAACAAACAGCCMACTACCGGCGGATTCAGACTAC 354
OY 244 AACGCTGTGAGAGACCCCGCGGCTGGGCGTTCATCATCACGCTTTCGTTTCTCTT 303
    || || || || || || || || || || || || || || || || || || || ||
Db 355 GACGCGCTGAGAGAGCGGCGGCGCTGCGCTCTTACACCGTGTGGCTGTGATT 414
OY 304 GTCTTGGTGTGATTTTGTACGTGTTTACCATCCCTGAGCAGACAAATTTGCC 363
    || || || || || || || || || || || || || || || || || || || ||
Db 415 GTCTGGGGGTGTTGATTTCTGCTGTCTGCTGACCAATTCAGAGATGTGAGACTGTG 474
OY 364 TCAAGTTCCTGTGATCTGAGATTCGATGATGATGATGATGATGATGATGATGATG 423
    || || || || || || || || || || || || || || || || || || || ||
Db 475 GAGACGTGGCTCTGTTACGTGAGACTTTGATTTTCACTTTGGAGCGGATTTGCT 534
OY 424 ATTGAACTGTGCTGCGGCTGTGTTGCGATATGAGAGATGAGAGAGAGAGAGAG 483
    || || || || || || || || || || || || || || || || || || || ||
Db 535 TTGAGATCTGGGCTGTGATTTGCTGCGCATPACAAAGGCTGGGCGGCGGAGCTAG 594
OY 484 TTTGCTGAAAGCCCTGCTGTATGATACATGCTTTTATCGCTTCAATGACAGTT 543
    || || || || || || || || || || || || || || || || || || || ||
Db 595 TTTGCCAGAGAGCCCTGTGATGTGACATCTTTGTGCTGATGCTGTGCGCAGTG 654
    || || || || || || || || || || || || || || || || || || || ||

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RESULT 7
 US-09-105-058C-19
 ; Sequence 19, Application US/09105058C
 ; Patent No. 640360
 ; GENERAL INFORMATION:
 ; APPLICANT: Blonar, Michael A.
 ; APPLICANT: Dwoletzky, Steven
 ; APPLICANT: Gridkoff, Valentin K.
 ; APPLICANT: Levesque, Paul C.
 ; APPLICANT: Little, Wayne A.
 ; APPLICANT: Neubauer, Michael G.
 ; APPLICANT: Yang, Wen-pin
 ; TITLE OF INVENTION: KCNQ POTASSIUM CHANNELS AND METHODS OF MODULATING SAME
 ; FILE REFERENCE: 3053-4052
 ; CURRENT FILING DATE: US/09/105,058C
 ; PRIOR FILING DATE: 1998-06-26
 ; PRIOR APPLICATION NUMBER: US 60/055,599
 ; NUMBER OF SEQ ID NOS: 28
 ; SOFTWARE: Patent In Ver. 2.1
 ; SEQ ID NO: 19
 ; LENGTH: 3287
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-09-105-058C-19

 Query Match 15.9%; Score 425; DB 4; Length 3287;
 Best Local Similarity 64.7%; Pred. No. 1, 2e-116;
 Matches 652; Conservative 0; Mismatches 345; Indels 0; Gaps 0

 QY 64 GGCCTGCTACTGCTGGGACACCCGGCGGCACGCCTGGTGGCGCGCGGCTGAGC 123
 Db 127 GCGCTTCGTGGGGGTGGACCCGGCGCCCGCCGACTCCACCGCGGAGCGCGCTGGATC 186
 QY 124 GAGAGCCGCGCGGAGCAAGCAGGGGCCCCGGATGAGCCTGCTGGGGAAGCCGCTCTTAC 183
 Db 187 GCGCGCTCCGAGGCGCCCAAGGCGGCGAGCATCCTCAGCAACCTCGCGGGGCGCGC 246
 QY 184 ACGAGTGCAGAGAGCTCGCGGCGCAAGTCAGAGCAGCGGGGGGCGAGACTACTGTAC 243
 Db 247 GCGCCCGGGAGACCCGCCCAAGCGCAAGCCCTTACCGCGAAGCTCAGAAATTCCTCTAC 306
 QY 244 AACGTGCTGAGAGACCCCGCGGCTGGGCGCTTCATCTACACAGCTTTCCTTCTCTCT 303
 Db 307 AACGTGCTGAGAGCGCGCGCGCGCTGGGCGCTTCATCTACACAGCGCTTCATCTCTCTG 366
 QY 304 GTCCTTGGTCTCTGATTTTGTCAAGTGTTCATCAATCCCTGAGCAGACAAATTTGGCC 363
 Db 367 GTTTCCTCCTCGCTCGCTGTCTGTCTGTTCACACATCAAGAGATAGAAAGAGCTCG 426
 QY 364 TCAAGTTCCTCTTGATCTGAGATTCGTGATGATTTGTCTGCTTTGGTTGGATTATC 423
 Db 427 GAGGCGGCGCTCTACATCTCGAAATCTGACTATCTGAGTTTGGCTGAGATCTTC 486
 QY 424 ATTGCATCTGCTCGCGGTTGCTGTGTGTGATTTAGAGATAGGAGCAAGACTGAG 483
 Db 487 GTCGGAATCTGGCGCGCAAGCGCTGCTGCGGATCCGCTGAGCCGGCTGAGGGCGGCTCAG 546
 QY 484 TTTCGTCGAAGACCCCTTCGTGTATAGATACATTTGTTATGCTTCATATAGCAGTT 543
 Db 547 TTTCGCGGAACCGTTCTGTGTATGATCAATAGTGCTCATGCGCTCCATTTGCGGTG 606
 QY 544 GTTTCGCAAAATCTAGGGTAAATTTTTCGACGCTCGCACTCAGAGTCTCGGTTTC 603
 Db 607 CTGGCGCGCGCTCCAGGCAACGCTTTTGCACATTCGCGCTCGGAGCCCTGCGCTTC 666
 QY 604 CTACAGATCTCGCTGCTGGGCGCATGAGCAAGGAGGAGGACTTGAATAATTAAGT 663
 Db 667 CTGCAATCTCTCGGATATATCCGATAGGAGACCGCGGGGAGGACCTGGAAGCTGCGGGC 726

OTHER INFORMATION: The thirteen nucleotides from 1691-1703 are

— ()

Query Match	15.9%	Score 423.4	DB 4	Length 3232
Best Local Similarity	64.6%	Pred. No. 5.6e-116		
Matches 631	Conservative 0	Mismatches 346	Indels 0	Gaps 0
QY	64	GCCTGCTACTGCTGGGACCCGCGCGCCACACGCTGTGGGGGGCGGGGCGTGGCTGAGG	123	
Db	194	GGCTTCGTCGGGGCTGGACCCCGCGCGGCCCACTCCACCCCGGAGGGGGCGCTGTGATC	253	
QY	124	GAGAGCCGCGCGGGGCAACGAGGGGGCCCGATGAGCCGTCTGGGGAACCGCCCTCTTAC	183	
Db	254	GCGGCTCCACAGGCCCCCAAGCCGCGGAGCATCTTCAGCAAAACCTCCGGGGGGGGCCG	313	
QY	184	ACGAGTAGCCAGAGACTCCGGGCGCACGTCAAGTACCGGGGGGTGCAGACTACTGTAC	243	
Db	314	GGGGCGGGAGAGCCCCCAAGCGCAAGCCCTTCAACGCGCAAGCGAAGTAATTTCTCTAC	373	
QY	244	AACGTGCTGGAGAGACCCCGCGCTGGGGCTGCATCTACCAACGCTTTCGTTTCTCCTT	303	
Db	374	AACGTGCTGGAGGCGCGCGCGCTGGGGCTTCACTACCAAGCTTACGTTTCTCTCTG	433	
QY	304	GTTTGTGGTGGCTGTAATTTGTTCAGTGTTTTCAACATCCCTAGCACACAAAAATGGCC	363	
Db	434	GTTTTCCTCGCTCGTGTGCTGTCTGTGTTTCCACATCAAGAGATATGAGAGAGCTCG	493	
QY	364	TCAAAGTTGCTCTGTATCCCTGGAGTTCGATGATGTGTCTTTGGTTTGGAGTTATC	423	
Db	494	GAGGGGGCCCTCTACATCCGGAATCGTACATATGTGTGTTTGGCGGTGAGTACTTC	553	
QY	424	ATTCAATGTGTCGTGGGGTGTCTGTTTCGATATAGAGATGGCAAGAAACATGAGG	483	
Db	554	GTCGGATATGGGCGGCAGAGCTGCTGCTCCGGTACCGTAGGCTGGAGGGGGCGGCTCAAG	613	
QY	484	TTTGTGCGAAACCCCTCGTGTGTATAGATACCATTGTTCTTATGCTTCAATAGCAGTT	543	
Db	614	TTTGGCCGGAACCCCTCTGTGTGATGTGACATCATGTGCTCATCGCTCCATATGGCGTG	673	
QY	544	GTTTCTGCAAAAACTCGAGGTATATTTTGGCAGCTGCAGCTAGAGTCTCCGTTTC	603	
Db	674	CTGGCGCGCGGTCCCAAGGCAAGCTTTTGGCAATCTGCGCCTCCGGAGCCTCTGGCTTC	733	

604 CTACAGATCCCTCCGATGTCGATGACCGAAGGAGGAGGACCTTGGAAATTAATCTGGGT 663
DB 734 CTGACAGATTTCTGGGATGATGATCCGATGACCGGAGGAGGACCTGAGAGCTGCTGGGC 793
OY 664 TCAGTGGTTATGCTCAGCAGAGAAATTAATCAGAGCTTGTGATGATTTTGGTT 723
DB 794 TCTGTGGTCTATGCCACAGCAGAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 853
OY 724 CTATATTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 783
DB 854 CTGATCCCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 913
OY 784 ACATATGAGATGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 843
DB 914 ACCTACGGGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 973
OY 844 AAACCTCCCTTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 903
DB 974 AAGTACCCCTCAGACCTGGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1033
OY 904 TCTTTCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 963
DB 1034 TCTTTCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1093
OY 964 CAACACCCGCGAAGACCTTTGAGAAAGAGAGAGACCCAGCTGCCAATCTGATTCAGTGT 1023
DB 1094 CAGCAGAGGAGCAGAGACCTTTGAGAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1153
OY 1024 GTTTGGCGTGTAGTACGC 1040
DB 1154 GCCTGGAGATTTCTACGC 1170

RESULT 9
US-09-177-650-95
Sequence 95, Application US/09177650
Patent No. 6413719
GENERAL INFORMATION:
APPLICANT: Leppert, Mark F.
APPLICANT: Singh, Nanda
APPLICANT: Charlier, Carole
TITLE OF INVENTION: KCMQ2 AND KCMQ3 - POTASSIUM CHANNEL GENES WHICH ARE
TITLE OF INVENTION: MUTATED IN BENIGN FAMILIAL NEONATAL CONVULSIONS (BFNC)
TITLE OF INVENTION: AND OTHER EPILEPSIES
FILE REFERENCE: 2323-134
CURRENT APPLICATION NUMBER: US/09/177,650
CURRENT FILING DATE: 1998-10-23
EARLIER APPLICATION NUMBER: 60/063,147
EARLIER FILING DATE: 1997-10-24
NUMBER OF SEQ ID NOS: 129
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 95
LENGTH: 3237
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (128)..(2917)
US-09-177-650-95

Query Match 15.9%; Score 423.4; DB 4: Length 3237;
Best Local Similarity 64.6%; Pred. No. 3.6e-116;
Matches 631; Conservative 0; Mismatches 346; Indels 0; Gaps 0;

OY 64 GCCTGTCTACTGTGCGGACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 123
DB 194 GCGTTCGTGGGCTGGACCCCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 253
OY 124 GAGAGCCCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 183
DB 254 GCGGCGCTCGAGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 313
OY 184 ACGAGTAGCCAGAGCTGCCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 243

DB 314 GCGCGCGGGAACCCCCCAAGGCGACGCTTCTACCGGAGAGCTGACAGAAATTTCTCTAC 373
OY 244 AACGTCTGAGAGAGACCCCGGCGGCTGGGCGTTCATCTACACAGCTTTTGTCTGCTTCT 303
DB 374 AAGGTCTGAG 433
OY 304 GCTTTGGTGTGATTTTGTGAGGTTTGTACCATCCCTGAGCAGACAAATTTGGCC 363
DB 434 GTTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 493
OY 364 TCAAGTTCCTCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 423
DB 494 GAGGCGGCGCTCTACATCTCTGGAATCTGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 553
OY 424 ATTGCAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 483
DB 554 GTGCGGATCTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 613
OY 484 TTTGCTGGAAGCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 543
DB 614 TTTGCGGGAACCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 673
OY 544 GTTTCTGCAAAAATCAGGCTAATTTTGTGCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 603
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OY 734 TCAGTGGTTATGCTCAGCAGAGAAATTAATCAGAGCTTGTGATGATTTTGGTT 723
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OY 1024 GTTTGGCGTGTAGTACGC 1040
DB 1154 GCCTGGAGATTTCTACGC 1170

RESULT 10
US-09-105-058C-3
Sequence 3, Application US/09105058C
Patent No. 6403360
GENERAL INFORMATION:
APPLICANT: Bianar, Michael A.
APPLICANT: Dmoretzky, Steven
APPLICANT: Grubkoff, Valentin K.
APPLICANT: Levesque, Paul C.
APPLICANT: Little, Wayne A.
APPLICANT: Neubauer, Michael G.
APPLICANT: Yang, Wen Pin
TITLE OF INVENTION: KCMQ2 AND KCMQ3 - POTASSIUM CHANNELS AND METHODS OF MODULATING SAME

FILE REFERENCE: 3053-4052
CURRENT APPLICATION NUMBER: US/09/105,058C
CURRENT FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: US 60/055,599
PRIOR FILING DATE: 1997-08-12
NUMBER OF SEQ ID NOS: 28
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3
LENGTH: 900
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: 900 nucleotides of human KCNQ2
US-09-105-058C-3

Query Match 15.8%; Score 421.4; DB 4; Length 900;
Best Local Similarity 68.6%; Pred. No. 6e-115;

Matches 581; Conservative 0; Mismatches 266; Indels 0; Gaps 0;

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QY 254 AGAGACCCCGCGGCTGGGGTTCATCACCACCGCTTTCGTTTCTCTGCTTGGTT 313
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QY 314 GCTTATTTTGTGAGTGTTCACATCCCTGAGCAGACAAATTTGGCTCAAGTTGCC 373
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QY 434 GGTCTGCGGTTGCTGTTCGATATAGAGATGCAAGAGAACAGAGAGTGTGTGAA 493
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Db 257 GGGCGCGAGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 316
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Db 497 ATGCGCAAGCAAGAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 556
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QY 734 CGTCTTCTTGTCTTATCTGTGTGAAAGATGCCAATTAAGATTTTCTATATATGAG 793
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QY 854 TAACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 913
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Db 677 AGACCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 736
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Db 737 CGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 796
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QY 974 AGAAACACTTTGAAAGAGAGAACCCAGCTGTGCAACCTCATCTATGTGTGTGTGT 1033
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Db 797 AGAAGCACTTTGAGAGAGGCGGAACCCGGCAGCAGCGCTGATCCAGTGGCGTGGAGAT 856
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Db 857 TTACGC 863
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RESULT 11

US-09-105-058C-5
Sequence 5, Application US/09105058C
Patent No. 6403360

GENERAL INFORMATION:

APPLICANT: Blahar, Michael A.
APPLICANT: Dworetzky, Steven
APPLICANT: Gridkoff, Valentin K.
APPLICANT: Levesque, Paul C.
APPLICANT: Little, Wayne A.
APPLICANT: Neubauer, Michael G.

TITLE OF INVENTION: KCNQ POTASSIUM CHANNELS AND METHODS OF MODULATING SAME

FILE REFERENCE: 3053-4052

CURRENT APPLICATION NUMBER: US/09/105,058C

PRIOR FILING DATE: 1998-06-26

PRIOR APPLICATION NUMBER: US 60/055,599

NUMBER OF SEQ ID NOS: 28

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 5

LENGTH: 900

TYPE: DNA

ORGANISM: mouse

OTHER INFORMATION: 900 nucleotides of murine KCNQ2

US-09-105-058C-5

Query Match 15.8%; Score 420.6; DB 4; Length 900;
Best Local Similarity 68.7%; Pred. No. 1e-115;

Matches 579; Conservative 0; Mismatches 264; Indels 0; Gaps 0;

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QY 204 GCGCAAGCTCAAGTACGCGGCGGTGACAGTCTGTACAAAGTGTGAGAGACCCG 263
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Db 27 GCGCAAGCTCTTACAGCCCAAGTACGAGAAATTCCTTACAAAGTGTGAGAGACCCG 86
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QY 264 CGGCTGGGCGTTCATCTACACAGCTTTCCTTCTCTCTCTCTCTCTCTCTCTCTCT 323
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Db 87 CGGCTGGGCGTTCATCTACACAGCTTTCCTTCTCTCTCTCTCTCTCTCTCTCTCTCT 146
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QY 444 TTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 503
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Db 327 TGTATATATACCATTTGTTTCTTATGCTTCAATATGACAGTTGTTTGTGCAAAATCTCAGG 386
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QY 564 TATATTTTGTGCACTGTGCACTCAAGATCTCCGTTTCTCAAGATCTCCGATGCT 623
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QY 684 CAAGAAATTAATCAAGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 743
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Oy	61	GACGGCTGTACTCTGTGGGCACCCGCGCGCCCAAGCTGTGGTGGCGGCGGAGGATGGGCTTG	120
Db	61	GACGGCTGTACTCTGTGGGCACCCGCGCGCCCAAGCTGTGGTGGCGGCGGAGGATGGGCTTG	120
Oy	121	AGGCAAGCCGCGCGGGGCAAGCAGGGGGCCCGGATGAGACCTGTGGGGAAGCCGCTCTCT	180
Db	121	AGGCAAGCCGCGCGGGGCAAGCAGGGGGCCCGGATGAGACCTGTGGGGAAGCCGCTCTCT	180

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RESULT 2
US-09-825-147-1
/ Sequence 1, Application US/09825147
/ Patent No. US20020042505A1
/ GENERAL INFORMATION:
/ APPLICANT: Hu, Yi
/ APPLICANT: Kieke, James Alvin
/ APPLICANT: Turner, C. Alexander Jr.
/ APPLICANT: Nehls, Michael C.
/ APPLICANT: Friedrich, Glenn
/ APPLICANT: Zambrowicz, Brian
/ APPLICANT: Sands, Arthur T.
/ TITLE OF INVENTION: No. US20020042505A1el Human Ion Channel Protein and
/ TITLE OF INVENTION: Polynucleotides Encoding the Same
/ FILE REFERENCE: LEX-0160-USA
/ CURRENT APPLICATION NUMBER: US/09/825,147
/ PRIOR FILING DATE: 2001-04-03
/ PRIOR APPLICATION NUMBER: US 60/194,255
/ NUMBER OF SEQ ID NOS: 3
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 1
/ LENGTH: 2772
/ TYPE: DNA
/ ORGANISM: homo sapiens
/ US-09-825-147-1

Query Match 99.8% Score 2662.2: DB 10: Length 2772:
Best Local Similarity 99.9%: Pred. No. 0:
Matches 2664: Conservative 0: Mismatches 3: Indels 0: Gaps 0:
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Db 346 TACAACGTGCTGGAGAGACCCCGGCGCTGGCGCTTCATCTACACGCTTTCGTTTCTC 405
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Oy 961 GAACAACCTCCCTAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1020
Db 1066 GAACAACCTCCCTAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1125
Oy 1021 TGTGTTGGGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1080
Db 1126 TGTGTTGGGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1185
Oy 1081 CACTTGAAGGCTTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1140
Db 1186 CACTTGAAGGCTTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1245
Oy 1141 GTGCGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1200
Db 1246 GTGCGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1305
Oy 1201 AGGAGGTCCCAACACGATATCAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1260
Db 1306 AGGAGGTCCCAACACGATATCAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1365
Oy 1261 TGAAGCTTCAACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 1320
Db 1366 TGAAGCTTCAACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 1425
Oy 1321 AAACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1380
Db 1426 AAACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1485
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QY	1381	TGCCAGTGATGATATGATAGTGAAGACCTTCACCCACCACTTAAACTTCATTCGAGCT	1440
Db	1486	TGCCAGTGATGATATGATAGTGAAGACCTTCACCCACCACTTAAACTTCATTCGAGCT	1545
QY	1441	ATCGAATTTATGAATTTTCATGTGGAAAAAGGAAATTAAGCAAAACGTTACGTCATAT	1500
Db	1546	ATCGAATTTATGAATTTTCATGTGGAAAAAGGAAATTAAGCAAAACGTTACGTCATAT	1605
QY	1501	GATGTAAAGATGCTCAGTAAACAAATTTCTGCTCATCTTGACATGTTGTAGAAAT	1560
Db	1606	GATGTAAAGATGCTCAGTAAACAAATTTCTGCTCATCTTGACATGTTGTAGAAAT	1665
QY	1561	AAAAGCCTTCAACACAGTGTATCAAAATTTTGGAAAAAGGCAAAATCAATCCAGATTAAG	1620
Db	1666	AAAAGCCTTCAACACAGTGTATCAAAATTTTGGAAAAAGGCAAAATCAATCCAGATTAAG	1725

[illegible]

Y	2041	GCAGTGGCACCCACCAACACCAATTGGTAAACCAATTAATACGGACCCAGGACGACGCC	2100
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Y	2101	CCACACCACTTTACAGATCCACCTCCTCTCCAGCAGTCAACCAATCTGCCCCAGGCCAGAA	2160
b	2206	CCACACCACTTTACAGATCCACCTCCTCTCCAGCAGTCAACCAATCTGCCCCAGGCCAGAA	2265
Y	2161	ACCTCTCACCCCTAACCCCTGCAGGCTTTACAGGAAGCAATTTGTGACGTCAACCACTGCTT	2220
b	2266	ACCTCTCACCCCTAACCCCTGCAGGCTTTACAGGAAGCAATTTGTGACGTCAACCACTGCTT	2325
Y	2221	GTTGCTCCAGGAAAAATGTTGAGGTTGCACAGTCAATCTCACCAAGGACCGTTCTATG	2280
b	2326	GTTGCTCCAGGAAAAATGTTGAGGTTGCACAGTCAATCTCACCAAGGACCGTTCTATG	2385
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b	2386	AGGAAAAAGTTTGACATGGGAGGAGAAAACTGTTGTCTGTCTGCCATGATGCCGAAG	2445
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b	2446	GACTTGGGCAATCTTTCTCTGTGCAAAAACCTGATCTCAGGTGCGACCGAGGAACCTGAATATA	2505
Y	2401	CAACTTTAGGAGATGAGTCAAGTGCGTCCAGAGGACGCCAAGATTTTAAACCCCAATGG	2460
b	2506	CAACTTTAGGAGATGAGTCAAGTGCGTCCAGAGGACGCCAAGATTTTAAACCCCAATGG	2565

QY	2461	AGGCATCCAAATTTGTTTATTAACATGATGAAGAGGTGGTCCGGAAGAGCAGAGACAGAC	2520
Db	2566	AGGGATATCAAAATTTGTTTATTAACGATGAGAGAGTGGTCCGGAAGAGCAGAGACAGAC	2625
QY	2521	ACTTTGATGGCCGACGGCGACCCCTGCCAGGAACTGCTTTGCATCAGACATCTCTAAG	2580
Db	2626	ACTTTTATGTCGCACGCCGACGCTGCCAGGGAAGCTTGCTTGCACTACAGACTCTTAAG	2685
QY	2581	ACTGGAAGGTACAGATCATCTCAGACATTTTGAAGCGCAGAGAAATGATAGTCCCTC	2640
Db	2686	ACTGGAAGGTACAGATCATCTCAGACATTTTGAAGCGCAGAGAAATGATAGTCCCTC	2745
QY	2641	AGCTTGCCATCATCAAACTGGAATTA	2667
Db	2746	AGCTTGCCATCATCAAACTGGAATTA	2772

RESULT 3
 US-09-825-147-3
 : Sequence 3, Application US/09825147
 : Patent No. US20020042505A1
 : GENERAL INFORMATION:
 : APPLICANT: Hu, Yi
 : APPLICANT: Kieke, James Alvin
 : APPLICANT: Turner, C. Alexander Jr.
 : APPLICANT: Nehls, Michael C.
 : APPLICANT: Friedrich, Glenn
 : APPLICANT: Zambrowicz, Brian
 : APPLICANT: Sands, Arthur T.
 : TITLE OF INVENTION: NO. US20020042505A1el Human Ion Channel Protein and
 : FILE REFERENCE: LEX-0160-USA
 : CURRENT APPLICATION NUMBER: US/09/825,147
 : CURRENT FILING DATE: 2001-04-03
 : PRIOR APPLICATION NUMBER: US 60/194,255
 : PRIOR FILING DATE: 2000-04-03
 : NUMBER OF SEQ ID NOS: 3
 : SOFTWARE: FastSeq for Windows Version 4.0
 : SEQ ID NO 3
 : LENGTH: 3111
 : TYPE: DNA
 : ORGANISM: homo sapiens
 : US-09-825-147-3

Query Match	99.8%	Score 2662.2	DB 10	length 3111
Best local Similarity	99.9%	Pred. No. 0		
Matches 2664	Conservative	0	Mismatches	3
			Indels	0
			Gaps	
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b	165	ATGAAGATGTGCAGTCTGGGCCGGGCAAGGTCTCTGAACCTCGCGCAGCCGACAGGGGC	224	
Y	61	GAGGCGCTCTACTGCTGGGCAACCCCGCGCACGCTGTGGGGGGGGGGGGGCTG	120	
b	225	GAGGCGCTCTACTGCTGGGCAACCCCGCGCACGCTGTGGGGGGGGGGGGGCTG	284	
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b	285	AGGAGAGACCGCGCGGCGCAAGAGAGGGGGCCGGATGACCTCTGTGGGAAACCGCTCT	344	
Y	181	TACAGCAGTAGCCAGAGCTCCGGGCGCAACGTCAAGTACCGCGGGGTGACGAACTACTG	240	
b	345	TACACAGTAGCCAGAGCTCCGGGCGCAACGTCAAGTACCGCGGGGTGCAAACTACTG	404	
Y	241	TACACAGTCTCTGGAGAGACCCCGGGGCTGGGCGTTCACTACACAGCTTTCGTTTTCTC	300	
b	405	TACACAGTCTCTGGAGAGACCCCGGGGCTGGGCGTTCACTACACAGCTTTCGTTTTCTC	464	
Y	301	CTTGTCTTGGTGGTCTATTGTGATGCTGTTTCTACATACCTTACAGCAGCAACAAATTG	360	
b	465	CTTGTCTTGGTGGTCTATTGTGATGCTGTTTCTACATACCTTACAGCAGCAACAAATTG	524	

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Db 1545 TGCAGTGTGATGTATACAGTGAAGACCTTACCCGACACTTAAACTGTCTATTCAGCT 1504
OY 1441 ATCAGAAATTAAGAAATTTATCTGTTGCAAAACGGAAGTTTAAAGAAACGTTACGCCATAT 1500
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Db 1785 AAGAGCGAGAGAAATTAACAGCAAGCAATGAGACCAAGACATGCTAGTATGCGGT 1844
OY 1681 CGGAGTGTCAAGGTTGAAAAAAGAGTACAGTCCATAGAGTCCAGCTGACCTCTACTA 1740
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Db 1965 CAGATCCGACCTTTTGAATGTGAACAGACATCTGACTATCAAAAGCCCTGTGGATAGCAAA 2024
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1921 TTATCCAGATCACTAGTGGCAACATCTCGAGAGCCCTGAGTTCACTTCTGAGCCCAAT 1980
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1981 GAGTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2040
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2041 GTGCGAATTTGTCAGAGCGATGGCTGAGCGAGCCAGCCAGCCAGCCAGCCAGCCAG 2100
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2221 AGCATTTCTGACGTCACACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2280
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2581 GCTGCTTTGTCAGATCTCTTAAGGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 2640
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Db 2641 AAGCAGAGAGAAATGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2694
RESULT 5
US-09-810-796-1
; Sequence 1, Application US/09810796
; Patent No. US20020102677A1
; GENERAL INFORMATION:
; APPLICANT: Jega, Timothy James
; APPLICANT: ICAGEN, Inc.
; TITLE OF INVENTION: KCNO5, a No. US20020102677A1 Potassium Channel
; FILE REFERENCE: 018512-005010US
; CURRENT APPLICATION NUMBER: US/09/810,796
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 60/190,954
; PRIOR FILING DATE: 2000-03-21
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 1
; LENGTH: 3071
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human outwardly rectifying, voltage-gated
; NAME/KEY: CDS
; LOCATION: (10)..(2703)
; OTHER INFORMATION: KCNO5-1
US-09-810-796-1
Query Match 98.5%; Score 2626.4; DB 10; Length 3071;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 2664; Conservative 1; Mismatches 2; Indels 27; Gaps 1;
Db 1 ATGAAGATGTGAGTGGGCGCGGCGAGGCTGCTGTAATCTGCGACGCCAGCGGCG 60
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DB 610 TTCTCAGATCTCCGATGCTGCGATGAGCCGAGGGAGGACATTGGAATTAATCTG 669
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DB 1270 GGCAGTCCCAAGAAAGTGCAGAGAGTGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1329
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QY 1414 CCACACCTTAAAGTGTATGAGAGTGCATGAGAAATTAATGAAATTTGATGCTGCTGCTGCT 1473
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QY 1594 GGAAGAGGCAATCAGATCAGATAGAGAGAGGAGAGAAATTAACAGCAACATGAG 1653
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QY 1774 GCTCAGGCTCTGCTTGGCTTTCATCTCAGATCCACCTTTTGAATGTGACAGATCT 1833
DB 1810 GCTCAGGCTCTGCTTGGCTTTCATCTCAGATCCACCTTTTGAATGTGACAGATCT 1869
QY 1834 GACTATCAAAAGCTCTGAGTATGAGCAAAAGATCTTGGGTTCCGCAAAAGAGTGTGCTC 1893
DB 1870 GACTATCAAAAGCTCTGAGTATGAGCAAAAGATCTTGGGTTCCGCAAAAGAGTGTGCTC 1929
QY 1894 TTATCCAGATCACTAGTGTGCAAGATCTGAGAGAGCTGCAAGTTCATTTGCAAGCAAT 1953
DB 1930 TTATCCAGATCACTAGTGTGCAAGATCTGAGAGAGCTGCAAGTTCATTTGCAAGCAAT 1989
QY 1954 GAGTTCAAGTCCGAGACTTTTACGCGCTTAGGCTTACTATGACAGTCAAGCAACAG 2013
DB 1990 GAGTTCAAGTCCGAGACTTTTACGCGCTTAGGCTTACTATGACAGTCAAGCAACAG 2049
QY 2014 GTGCCAATTTAGTCAAGAGGATGCTCAGCAGTGGCAGGCGCACCAACCATTTGCAAGCA 2073
DB 2050 GTGCCAATTTAGTCAAGAGGATGCTCAGCAGTGGCAGGCGCACCAACCATTTGCAAGCA 2109
QY 2074 ATAAATACGGCACCAGCAAGCAGAGAGCCCAACACTTTACAGATCCACCTCTCTCCA 2133
DB 2110 ATAAATACGGCACCAGCAAGCAGAGAGCCCAACACTTTACAGATCCACCTCTCTCCA 2169
QY 2134 GCCATCAAGATCTGCGCCAGGCGCAAGAACTGTGACACCTTAACCTGTGAGAGAA 2193
DB 2170 GCCATCAAGATCTGCGCCAGGCGCAAGAACTGTGACACCTTAACCTGTGAGAGAA 2229
QY 2194 AGCATTTCTGACGTACACACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2253
DB 2230 AGCATTTCTGACGTACACACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2289
QY 2254 TCAATATCTACCAAGAACCGTTCTATGAGAGAAAGCTTTGACATGGAGAGAACTCTG 2313
DB 2290 TCAATATCTACCAAGAACCGTTCTATGAGAGAAAGCTTTGACATGGAGAGAACTCTG 2349
QY 2314 TTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2373
DB 2350 TTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2409
QY 2374 ATCAGTTCGACCGAGAACTGATATACAACTTTCAGGAGTGAAGTCAAGTGCCTCAGA 2433
DB 2410 ATCAGTTCGACCGAGAACTGATATACAACTTTCAGGAGTGAAGTCAAGTGCCTCAGA 2469
QY 2434 GGCAGCCCAAGATTTTACCCCAATGAGAGATCCAAATTTGTTATTAAGTATGAGAG 2493
DB 2470 GGCAGCCCAAGATTTTACCCCAATGAGAGATCCAAATTTGTTATTAAGTATGAGAG 2529
QY 2494 GTGGGTCCCGAAGAGAGAGAGACACTTTGATGCGGACCGAGCCGCGCAAGGAA 2553
DB 2530 GTGGGTCCCGAAGAGAGAGAGACACTTTGATGCGGACCGAGCCGCGCAAGGAA 2589
QY 2554 GCTGCTTTTGCATCAGACTCTTAAGAGCTGGAAGTTCAGAGTATCATGACAGATTTGT 2613
DB 2590 GCTGCTTTTGCATCAGACTCTTAAGAGCTGGAAGTTCAGAGTATCATGACAGATTTGT 2649
QY 2614 AAGGAGAGAAAGTACAGATGCTTCAAGTGTGCTTCAATGCTCAAGTGAATTA 2667
DB 2650 AAGGAGAGAAAGTACAGATGCTTCAAGTGTGCTTCAATGCTCAAGTGAATTA 2703

RESULT 6
US-09-813-148-1
; Sequence 1, Application US/09813148
; Patent No. US20020076809A1

```

GENERAL INFORMATION:
APPLICANT: STEINMEYER, Klaus
APPLICANT: LERCHE, Christian
APPLICANT: SCHERER, Constanze
APPLICANT: SEEBOM, Guisard
APPLICANT: BUSCH, Andreas E.
TITLE OF INVENTION: POTASSIUM CHANNEL PROTEIN KCND5, A NEW TARGET FOR DISEASES OF THE
TITLE OF INVENTION: NERVOUS SYSTEM AND CARDIOVASCULAR SYSTEM
FILE REFERENCE: 38005-119
CURRENT APPLICATION NUMBER: US/09/813,148
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: DE 100 13 732.6
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: US 60/194,041
PRIOR FILING DATE: 2000-04-03
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn version 3.0
SEQ ID NO: 1
LENGTH: 3074
TYPE: DNA
ORGANISM: Homo sapiens
US-09-813-148-1

Query Match      98.1%   Score 2617.2   DB 10:   Length 3074:
Best Local Similarity 98.7%   Pred. No. 0:
Matches 2659:   Conservative 0:   Mismatches 8:   Indels 27:   Gaps 1:

OY 1  ATGAGGATGTCGATCGGGCCGCGGAGAGGTCGTCGTAACCTCGGACGCCAGGGGC 60
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DB 215 ATGAGGATGTCGATCGGGCCGCGGAGAGGTCGTCGTAACCTCGGACGCCAGGGGC 274
OY 61  GACGGCTGCTACTGCTGGGCAACCCGCGGCGCAGCCTTGCTGGCGCGCGGTGGCC 120
    |||||||
DB 275 GACGGCTGCTACTGCTGGGCAACCCGCGGCGCAGCCTTGCTGGCGCGCGGTGGCC 334
OY 121 AGGAGAGCGCGCGGCGGCAAGCAGGCGCGCGGAGGCTGCTGGGAAAGCCCTCTCT 180
    |||||||
DB 335 AGGAGAGCGCGCGGCGGCAAGCAGGCGCGCGGAGGCTGCTGGGAAAGCCCTCTCT 394
OY 181 TACACAGTAGCCAGAGCTGCCGCGCAACGTCAGTACCGCGCGGTGCAGACTACCTG 240
    |||||||
DB 395 TACACAGTAGCCAGAGCTGCCGCGCAACGTCAGTACCGCGCGGTGCAGACTACCTG 454
OY 241 TACACAGTAGCCAGAGCTGCCGCGCAACGTCAGTACCGCGCGGTGCAGACTACCTG 300
    |||||||
DB 455 TACACAGTAGCCAGAGCTGCCGCGCAACGTCAGTACCGCGCGGTGCAGACTACCTG 514
OY 301 CTGTCTTTGCTGCTGATTTTGTCAAGTCTTTTCAACATCCCTGAGCACAAATTTG 360
    |||||||
DB 515 CTGTCTTTGCTGCTGATTTTGTCAAGTCTTTTCAACATCCCTGAGCACAAATTTG 574
OY 361 GCCCTCAAGTTCCTTCTGATTCCTGAGTCTGATGATGATGCTGCTTTGGTTTGAGTTG 420
    |||||||
DB 575 GCCCTCAAGTTCCTTCTGATTCCTGAGTCTGATGATGATGCTGCTTTGGTTTGAGTTG 634
OY 421 ATCATTTGAATCTGCTGCGGGTTCGCTGTTGTCGATATAGAGATGCGCAAGAGACTG 480
    |||||||
DB 635 ATCATTTGAATCTGCTGCGGGTTCGCTGTTGTCGATATAGAGATGCGCAAGAGACTG 694
OY 481 AGGTTGCTGGAAGCCCTTCTGTTATATATACATGTTTCTTATGCTTCATATAGCA 540
    |||||||
DB 695 AGGTTGCTGGAAGCCCTTCTGTTATATATACATGTTTCTTATGCTTCATATAGCA 754
OY 541 GTTCTTTCTGCAAAACTCAGGTAATATTTTGTGCACGCTGCACTAGAACTCCGT 600
    |||||||
DB 755 GTTCTTTCTGCAAAACTCAGGTAATATTTTGTGCACGCTGCACTAGAACTCCGT 814
OY 601 TTCTTACAGATCTCTCGCATGCTGCGCATGACCGAAGGGGAGGACCTGGAATTTACTG 660
    |||||||
DB 815 TTCTTACAGATCTCTCGCATGCTGCGCATGACCGAAGGGGAGGACCTGGAATTTACTG 874
OY 661 GGTTCAGGTTTATGTCACAGCAAGAAATTAATCAGCTTGTGATACATAGGATTTTGT 720
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DB 875 GGTTCAGGTTTATGTCACAGCAAGAAATTAATCAGCTTGTGATACATAGATTTTGT 934
OY 721 GTTCTTATTTTGTCTCTTCTTCTGATCTGATCTGATCTGATCTGATCTGATCTGATCT 780
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DB 935 GTTCTTATTTTGTCTCTTCTTCTGATCTGATCTGATCTGATCTGATCTGATCTGATCT 994
OY 781 TCTCATATGAGATGCTCTGCTGGGCGCAATTTACATTTGACAACTATTTGCTATGGA 840
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DB 995 TCTCATATGAGATGCTCTGCTGGGCGCAATTTACATTTGACAACTATTTGCTATGGA 1054
OY 841 GACAAACTCCCTTACTGCTGCTGGGAAAGATTGCTTTCTGAGAGCTTTGCACTCTTGGC 900
    |||||||
DB 1055 GACAAACTCCCTTACTGCTGCTGGGAAAGATTGCTTTCTGAGAGCTTTGCACTCTTGGC 1114
OY 901 ATTTCTTTCTTTGACCTTCTGCGGCAATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
    |||||||
DB 1115 ATTTCTTTCTTTGACCTTCTGCGGCAATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1174
OY 961 GAACAACACCGCCAGAAACACTTTGAGAAAGAGAAAGAAAGAAAGAAAGAAAGAAAGAA 1020
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DB 1175 GAACAACACCGCCAGAAACACTTTGAGAAAGAGAAAGAAAGAAAGAAAGAAAGAAAGAA 1234
OY 1021 TGTGTTTGGCGTATGTTACGACGCTGATGAGAAATCTGTTCCATTGCAACTGGAAGCA 1080
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DB 1235 TGTGTTTGGCGTATGTTACGACGCTGATGAGAAATCTGTTCCATTGCAACTGGAAGCA 1294
OY 1081 CACTTGAAGGCTTGGACACCTGCAACCTTACCA----- 1115
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DB 1295 CACTTGAAGGCTTGGACACCTGCAACCTTACCAAGAAAGAAAGAAAGAAAGAAAGAAAG 1354
OY 1116 --TCAGAGCTAAGTTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 1173
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DB 1355 AGTCAGAGCTAAGTTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 1414
OY 1174 AACAGCGGACAAACCTCAGTAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1233
    |||||||
DB 1415 AAGAGCGGACAAACCTCAGTAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1474
OY 1234 GGCAGTCCACCAAGTTCGAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1293
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DB 1475 GGCAGTCCACCAAGTTCGAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1594
OY 1294 TCGGTGCGCCTCAAAAGTTCGAGCCCAAAACAGTGTATGATGATGATGATGATGATGATG 1353
    |||||||
DB 1535 TCGGTGCGCCTCAAAAGTTCGAGCCCAAAACAGTGTATGATGATGATGATGATGATGATG 1594
OY 1354 ACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1413
    |||||||
DB 1595 ACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1654
OY 1414 CCACCACTTAAACCTGATTCGAGCTATGAGATGATGATGATGATGATGATGATGATGATG 1473
    |||||||
DB 1655 CCACCACTTAAACCTGATTCGAGCTATGAGATGATGATGATGATGATGATGATGATGATG 1714
OY 1474 AAGTTTAAAGAAAGTTCAGTCCATATGATGATGATGATGATGATGATGATGATGATGATG 1533
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DB 1715 AAGTTTAAAGAAAGTTCAGTCCATATGATGATGATGATGATGATGATGATGATGATGATG 1774
OY 1534 GGTCTATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1593
    |||||||
DB 1775 GGTCTATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1834
OY 1594 GGAAGAGGCAAAATACATCAGATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1653
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DB 1835 GGAAGAGGCAAAATACATCAGATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1894
OY 1654 ACCACAGAGATCTAGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1713
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DB 1895 ACCACAGAGATCTAGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1954
OY 1714 ATAGAGTCCAGAGTGAAGTCTAGTATGATGATGATGATGATGATGATGATGATGATGATG 1773
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DB 1955 ATAGAGTCCAGAGTGAAGTCTAGTATGATGATGATGATGATGATGATGATGATGATGATG 2014
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QY 1774 GCGTCAGCCCTGCTTGGCTTCATTCAGATCCACCTTTTGAATGTGAACAGACATCT 1833
 Db 2015 GCGTCAGCCCTGCTTGGCTTCATTCAGATCCACCTTTTGAATGTGAACAGACATCT 2074
 QY 1834 GACTTCAAAAGCCCTGTGGATAGCAAAAGATCTTGGGTGCGCAAAAGAGTGGCTGC 1893
 Db 2075 GACTTCAAAAGCCCTGTGGATAGCAAAAGATCTTGGGTGCGCAAAAGAGTGGCTGC 2134
 QY 1894 TTATCCAGATCACTAGTGGCCCAATCTGAGAGGCGCTGCAATTTATCTGAGCCCAAT 1953
 Db 2135 TTATCCAGATCACTAGTGGCCCAATCTGAGAGGCGCTGCAATTTATCTGAGCCCAAT 2194
 QY 1954 GAGTTCACTGCGCCAGACTTTCTAGCGCTTAGCCCTACTATGCAAGTCAACACAG 2013
 Db 2195 GAGTTCACTGCGCCAGACTTTCTAGCGCTTAGCCCTACTATGCAAGTCAACACAG 2254
 QY 2014 GTGCAATTTAGTCAAAAGGATGGCTGACAGATGGCAGCCACCAACCACTTGCACCA 2073
 Db 2255 GTGCAATTTAGTCAAAAGGATGGCTGACAGATGGCAGCCACCAACCACTTGCACCA 2314
 QY 2074 ATAAATAGCGACCCCAAGCCAGACCCCAACTTTAGATGCCATCCCTGCTCTCCA 2133
 Db 2315 ATAAATAGCGACCCCAAGCCAGACCCCAACTTTAGATGCCATCCCTGCTCTCCA 2374
 QY 2134 GGCATCAAGATCTGCGCCAGCCAGCAAACTTGCACCCCTAACCCTGACAGCTTACAG 2193
 Db 2375 GGCATCAAGATCTGCGCCAGCCAGCAAACTTGCACCCCTAACCCTGACAGCTTACAG 2434
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 Db 2435 AGCATTTCTAGCTCAACACCTGCTTGGCTTCCCAAGAAAATGTTCAGAGTTGCACAG 2494
 QY 2254 TCAAACTCAACCAAGAACGCTTATAGAGAAAAGCTTTGACATGGAGAGAGAACTCTG 2213
 Db 2495 TCAAACTCAACCAAGAACGCTTATAGAGAAAAGCTTTGACATGGAGAGAGAACTCTG 2554
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 Db 2555 TTGCTGTCTGCCATGGTGGCGAAGACTTGGGCAAACTTTGCTGTGCAAACTCTG 2614
 QY 2374 ATCAGGTGACCGAGAACTGAATATACAACTTTCAGGAGTGAAGTGGCTGCACAG 2433
 Db 2615 ATCAGGTGACCGAGAACTGAATATACAACTTTCAGGAGTGAAGTGGCTGCACAG 2674
 QY 2434 GGCACCCCAAGATTTTACCCCAATGGAGGAAATCCAAATTTGTTTAACTGATGAAG 2493
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 QY 2494 GTGGTCCCGAAGAGACAGACACTTTTATGGCGCACCGCAGCTGCCAGGGGA 2553
 Db 2735 GTGGTCCCGAAGAGACAGACACTTTTATGGCGCACCGCAGCTGCCAGGGGA 2794
 QY 2554 GCTGCTTTGATGATGATCTCTAAGACTGGAAGTCAAGTCACTGCAAGACTTTGT 2613
 Db 2795 GCTGCTTTGATGATGATCTCTAAGACTGGAAGTCAAGTCACTGCAAGACTTTGT 2854
 QY 2614 AAGCAGAGAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2667
 Db 2855 AAGCAGAGAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2908

RESULT 7
 US-10-128-870-22
 ; Sequence 22, Application US/10128870
 ; Patent No. US20020168724A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Blau, Michael A.
 ; APPLICANT: Dworetzky, Steven
 ; APPLICANT: Gribokoff, Valentin K.
 ; APPLICANT: Levesque, Paul C.
 ; APPLICANT: Little, Wayne A.
 ; APPLICANT: Neubauer, Michael G.

; APPLICANT: Yang, Wen-Pin
 ; TITLE OF INVENTION: KNO POTASSIUM CHANNELS AND METHODS OF MODULATING SAME
 ; FILE REFERENCE: DCS641V
 ; CURRENT APPLICATION NUMBER: US/10/128,870
 ; CURRENT FILING DATE: 2002-04-24
 ; PRIOR APPLICATION NUMBER: 09/105,058
 ; PRIOR FILING DATE: June 26, 1998
 ; PRIOR APPLICATION NUMBER: 60/055,599
 ; PRIOR FILING DATE: August 12, 1997
 ; NUMBER OF SEQ ID NOS: 28
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 22
 ; LENGTH: 2169
 ; TYPE: DNA
 ; ORGANISM: MOUSE
 ; US-10-128-870-22

Query Match 17.8%; Score 475.6; DB 9; Length 2169;
 Best Local Similarity 57.0%; Pred. No. 6.7e-130;
 Matches 1022; Conservative 0; Mismatches 664; Indels 108; Gaps 4;

QY 64 GGCCTGCTACTGCTGGGCGCCGCGGCGCCACGCTTGGTGGCGGCGGCGTGGAG 123
 Db 67 GGCCTGCTGGGCGCTGGACCCGCGCGCGCGCTGCACACCGCGCGCTACTCATC 126
 QY 124 GAGAGCGCGCGGCGCAAGCAGGCGCGCGATGAGCTGCTGGGGAAGCGCGCTCTTAC 183
 Db 127 GCGGGCTCCGAGCGCCCAAGCGCGCGAGCTTTGAGCAAGCGCGGAGCGGCGCG 186
 QY 184 ACGATGACGAGAGCTCCGCGCGCAAGCTCAAGTACCGCGGCGCGCAAGCTACTTAC 243
 Db 187 GAGCGCGGGAAGCGCCCGAAGCGCAAGCTTCAACCGCAAGCTGCGAAGATTCCTTAC 246
 QY 244 AAGCTGCTGAGAGACCGCGCGCGCTGCTGCTTCAACCGCTTCTGCTTCTCT 303
 Db 247 AAGCTGCTGAGAGCGCGCGCGCGCTGCTGCTTCAACCGCTTCTGCTTCTCT 306
 QY 304 GCTTTGCTGCTGCTGCTTGTGCTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTG 363
 Db 307 GCTTTGCTGCTGCTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGT 366
 QY 364 TCAAGTTCCTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTG 423
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 QY 424 ATTGCAATCTGCTGCGGCTGCTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTG 483
 Db 427 GTGAGATCTGCTGCTGCAAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 486
 QY 484 TTGCTCGAAGACCGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGT 543
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 Db 547 CTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 606
 QY 604 CTACAGATCTCCGAGATGGTGGGATGAGCCGAGGAGGAGGAGGAGGAGGAGGAGG 663
 Db 607 TTGCAATCTGCGGATGATCCGATGAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAG 666
 QY 664 TCAGTGGTTATGCTCAGCAGCAAGAAATTAATCAAGCTGCTGCTGCTGCTGCTGCT 723
 Db 667 TCGGTAGTCTACGCTCAGCAGCAAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 726
 QY 724 CTATTTTGTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 783
 Db 727 CTCTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 786
 QY 784 ACATATGAGATGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 843
 Db 787 ACCTACGAGATGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 846

844 AAACCTCCCTAACTTGGCTGGAGATGCTTTCGACAGCTTTCGACCTCTGGCAT 903
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 907 TCGTTCTTGGCTCTCGCTGCTGCTTGGGATTCGCGCTTGGCTGGAAGTCCAGAG 966
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 967 CAGCATCGGCAAAACCTTGGAGAAAGGAGAACCTTGGCGGAGCTGATCCAGTCT 1026
 1024 GTTTGGCTAGTATGACAGCAGTATGAGAAATCTGTTTCATTGCAACCTGGAAGCCAC 1083
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 1084 T----- 1084
 1087 TACGAGGAGACATCCTGCTCCCATGTACAGACTATCCACCTTGAACCAAGCTGGAG 1146
 1085 -----TGAAGGCTTGCACACCTGC 1104
 1147 CTGCTGAGGATCTCAAGAGCAATCTGACCTCAGCAAGAGGAGCCAGCCAGAG 1206
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 1207 CCATTCACCAAGTGAAGAGCTGTTGAAAGATGCTGTTCTTCACGACCCCGAGGCA 1266
 1162 GGCAGAGTATTAAGAGCCGACAAAGCTCAGTATGATGACAGAGAGTCCGACAGCCAG 1221
 1267 GCTGCCAAGGAAAGGCTCTCCCGAGCCAGAGCGTCCGCGGCTCCCGACAGTGGAT 1326
 1222 ATCAGACCGAGGAGCTCCACCAAGTGCAGAGAGCTGAGACTTCACAGACCGAACC 1261
 1327 CAGAGTCTTATGACAGCCGAGAGAGTCCGCAAGAGCTGAGAGCTTGGTACCGGAGC 1386
 1282 CGCTCCGCGGCTCGCTGCTGCTCAAAAGTTCTCAGCCAAACAGATGATGATGATGAC 1341
 1387 CGCAGACGAGGCTTTCGAGATTAAGAGTCTCATCCGCGAGAAATTCAGAAAGCAAGC 1446
 1342 ACAGCCCTGACCTGATGATATGATGATAAAAGAGAGCCAGTGTGATGATGATGATG 1401
 1447 C---TCCCTGGGAGAGCATGCTGAGAGCAACAAGAGCTTAAGCTGAGCTTGTGACT 1503
 1402 GAGACCTACCCACCACTTAAGAGTCTCATGAGCTATCAGATTAAGAAATTTGAT 1461
 1504 GAAAGATCTTACCTGCTGCTCAAAAGTATGACAGAGCTGTGTATGATGCTGCTTGG 1563
 1462 GTTCAAAAGAGAGTTTAAAGAAAGCTTACGCTCATATGATGATGATGATGATGATG 1521
 1564 GTATCTAAGCAAAAGTTCAAGAGAGTCTGCGCCATATGATGATGATGATGATGATG 1623
 1522 CAATATCTGCTGCTGATCTGAGACATGTTGTGTAGATTTAAAGCTTCAAAACAGTGT 1581
 1624 CAGTACTGCTGAGACATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1683
 1592 GATCAAAATTTTGGAGAAAGGCAATTCATCAGATTAAGAGAGCGGAGAGAAATTAACA 1641
 1664 GACCAAGATTTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1740
 1741 GGGGAAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1800
 1702 CAGGTACAGTCTATGAGATGCAAGCTGACAGCTGCTACTGACATGATCATGACAG 1755
 1801 CAGGCTCTGCTCATGAGAAAGAGCTGCACTTCTGCTGAGCATCTATACACAG 1854

RESULT 8
 US-10-128-870-1
 ; Sequence 1, Application US/10128870
 ; Patent No. US20020168724A1

GENERAL INFORMATION:
 APPLICANT: Blonar, Michael A.
 APPLICANT: Dworetzky, Steven
 APPLICANT: Gribkoff, Valentin K.
 APPLICANT: Levesque, Paul C.
 APPLICANT: Little, Wayne A.
 APPLICANT: Neuberger, Michael G.
 APPLICANT: Yang, Wen-Pin
 TITLE OF INVENTION: KNOX POTASSIUM CHANNELS AND METHODS OF MODULATING SAME
 FILE REFERENCE: DC584dV
 CURRENT APPLICATION NUMBER: US/10/128,870
 PRIOR APPLICATION NUMBER: 09/105,058
 PRIOR FILING DATE: June 26, 1998
 PRIOR APPLICATION NUMBER: 60/055,599
 PRIOR FILING DATE: August 12, 1997
 NUMBER OF SEQ ID NOS: 28
 SOFTWARE: Patentin Ver. 2.1
 SEQ ID NO: 1
 LENGTH: 896
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE: Description of Artificial Sequence: Consensus
 OTHER INFORMATION: nucleotide sequence as shown in Fig. 16A-16D
 FEATURE: y=c or t; r=a or g; m=a or c; k=g or t; s=g or c;
 OTHER INFORMATION: w=a or t; h=a, c, or t; b=g, t, or c; v=g, c, or a
 US-10-128-870-1
 Query Match 17.5%; Score 465.4; DB: 9; Length 896;
 Best Local Similarity 53.7%; Pred. No. 3.6e-127;
 Matches 460; Conservative 231; Mismatches 162; Indels 4; Gaps 2;
 190 AGCCAGAGCTCCCGGCAAGCTGACAGTACCGGCGGAGAGAGTCTTACAGCTG 249
 13 RGSMSCCMSYSAAGMGAACGCCWSTACCGSMRSMSCARMTTSMTCACAGCYS 72
 250 CTGAGAGAGCCCGGCGGCTGGGCTTCATCTACCAAGCTTTCCTGTTTCTCTT 309
 73 CTGAGAGAGCCCGGCGGCTGGGCTTCATCTACCAAGCTTTCCTGTTTCTCTT 132
 310 GATTGCTGATTTTGTGAGTGTCTTTCACCATCCCTGAGGACACAAATTTGCCCAT 369
 133 KSTCCYBTRKCTGCTGTS-YKWCACMMTCAAGAGTATGACAAAKRYTCBGRGRS 191
 370 TGCCCTTGATCTGAGAGTGTGATGATGATGATGATGATGATGATGATGATGATG 429
 192 KSSCTYMSWIMYTGAARAYMTKRCYATYKTSRYVTYGGHGBAGTWKYKTMGR 251
 430 ATCTGCTGCGGCTTGTGCTGTTGCTGATATAGAGATGAGCAAGAGAGTGGTGGT 489
 252 ATCTGCGGCGGCTTGTGCTGTTGCTGATATAGAGATGAGCAAGAGAGTGGTGGT 311
 490 GCAAGAGCCCTGCTGCTGTTTATAGATCAATTTCTTATGCTTCAATAGACAGTGT 549
 312 MCGAAGCCCTGCTGCTGTTTATAGATCAATTTCTTATGCTTCAATAGACAGTGT 371
 550 GCAAAAGTCAAGGATATATTTTGGCAGCTGCTGACCTAGAGTCTCCGTTCCAGAG 609
 372 GYBGHMMCCARGGCAAYTYTKGACVTCY---CTBCGRAGCTYGGSTYTCRCA 428
 610 ATCTGCTGCGGCTTGTGCTGTTGCTGATATAGAGATGAGCAAGAGAGTGGTGGT 669
 429 ATYTTGCGATGCTGCTGCTGTTTATAGATCAATTTCTTATGCTTCAATAGACAG 488
 670 GTTATGCTGACAGCAAGATTAATACAGAGCTTGTATACATAGATTTTGTCTTAT 729
 489 KCTCRIGCTCAGCAAGARACRSTRSACKGCTGAGATATGCTTCTBMSHCTCAT 548
 730 TTTTGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 789
 549 CTCKCYCTRTTYCTKSTACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 608


```

? Patent No. US20020168724A1
? GENERAL INFORMATION:
?
? APPLICANT: Blonar, Michael A.
? APPLICANT: Dworetzky, Steven
? APPLICANT: Glikboif, Valentin K.
? APPLICANT: Levesque, Paul C.
? APPLICANT: Little, Wayne A.
? APPLICANT: Neubauer, Michael G.
? APPLICANT: Yang, Wen-pin
?
? TITLE OF INVENTION: KCNO POTASSIUM CHANNELS AND METHODS OF MODULATING SAME
?
? FILE REFERENCE: DC56adiv
?
? CURRENT APPLICATION NUMBER: US/10/128,870
?
? CURRENT FILING DATE: 2002-04-24
?
? PRIOR APPLICATION NUMBER: 09/105,058
?
? PRIOR FILING DATE: June 26, 1998
?
? PRIOR APPLICATION NUMBER: 60/055,599
?
? PRIOR FILING DATE: August 12, 1997
?
? NUMBER OF SEQ ID NOS: 28
?
? SOFTWARE: Patentln Ver. 2.1
?
? SEQ ID NO 3
?
? LENGTH: 900

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; LENGTH: 900

TYPE: DNA
ORGANISM: Homo sapiens
FEATURE: 581; Conservative 0; Mismatches 266; Indels 0; Gaps 0;
OTHER INFORMATION: 900 nucleotides of human KCNQ2
US-10-128-870-3

Query Match 15.8%; Score 421.4; DB 9; Length 900;
Best Local Similarity 68.6%; Pred. No. 3.7e-114;
Matches 581; Conservative 0; Mismatches 266; Indels 0; Gaps 0;

194 AGAGCTGCGGCGCAACGTCACCTACCGGGGTGCGAGACTACCTTACAAAGTGGT 253
17 ACCCCCCCAAGCGCAAGCTTCTACCGCAAGCTGCAAGATTCCTCTACAACTGCTGG 76
254 AGAGACCGCGGCGGCGGCTGTCACCAAGCTTCTGCTTCTCTCTCTCTCTCTCT 313
77 AGCGGCGCGGCGGCTGCGGCTTATCTACCAAGCTGCTGCTCTCTCTCTCTCTCT 136
314 GCTTGAATTTGTCAGTGTTCACATTCCTGAGCAACAAATTTGGCTTCAAGTTCC 373
137 GCTGCTGCTGCTGCTGCTTTCACCAAGATGATGAGAAAGCTCGAGGCGGCGCC 196
374 TCTTGAATTCGAGTTCGATGATGATGATGATGATGATGATGATGATGATGAT 433
197 TCTTGAATTCGAGTTCGATGATGATGATGATGATGATGATGATGATGATGAT 256
434 GCTTGAATTCGAGTTCGATGATGATGATGATGATGATGATGATGATGATGAT 493
257 GCGGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 316
494 AGCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 553
317 AACCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 376
554 AACCTGAGGTAATTTTTCGCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 613
377 GCTTGAATTCGAGTTCGATGATGATGATGATGATGATGATGATGATGATGAT 436
614 TCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 673
437 TCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 496
674 ATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 733
497 ATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 556
734 GCTTGAATTCGAGTTCGATGATGATGATGATGATGATGATGATGATGATGAT 793
557 CCGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 616
794 ATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 853
617 ATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 676
677 AGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 736
914 CAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 973
737 CGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 796
974 AGAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1033
797 AGAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 856
1034 GTTACG 1040
857 TTTACG 863

Sequence 5, Application US/10128870
Patent No. US20020168724A1
GENERAL INFORMATION:
APPLICANT: Blana, Michael A.
APPLICANT: Dworetzky, Steven
APPLICANT: Gribkoff, Valentin K.
APPLICANT: Levesque, Paul C.
APPLICANT: Little, Wayne A.
APPLICANT: Neubauer, Michael G.
TITLE OF INVENTION: KCNQ POTASSIUM CHANNELS AND METHODS OF MODULATING SAME
FILE REFERENCE: DC58ADIV
CURRENT FILING DATE: 2002-04-24
PRIORITY FILING DATE: 09/105,058
PRIORITY FILING DATE: June 26, 1998
PRIORITY FILING DATE: 60/055,599
PRIORITY FILING DATE: August 12, 1997
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 5
LENGTH: 900
TYPE: DNA
ORGANISM: MOUSE
FEATURE:
OTHER INFORMATION: 900 nucleotides of murine KCNQ2
US-10-128-870-5

Query Match 15.8%; Score 420.6; DB 9; Length 900;
Best Local Similarity 68.7%; Pred. No. 6.4e-114;
Matches 579; Conservative 0; Mismatches 264; Indels 0; Gaps 0;

204 GCGCAAGCTGCAAGTTCACCGGCGGCTGCAAGTTCACCGGCTGCAAGTTCAC 263
27 GCGCAAGCTGCAAGTTCACCGGCGGCTGCAAGTTCACCGGCTGCAAGTTCAC 86
264 GCGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 323
87 GCGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 146
324 GTCAGTGTTCGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 383
147 TTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 206
384 GCGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 443
207 GCGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 266
444 TTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 503
267 CTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 326
504 TTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 563
327 TTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 386
564 TTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 623
387 CTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 446
624 GCGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 683
447 CTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 506
684 CTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 743
507 CTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 566
744 TTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 803
567 GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 862
804 GTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 863

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Db      627 GTGGGCTGTGATCACCTGTACACCATTTGGCTACGGGGACAACTACCTGTAGACCTGGAA 686
      |||||  ||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Qy      864 GGGAGATTGCTTTCTGCAAGGCTTTGCACCTCTTGGCAATTTCTTTCTTCCACTTCCTGC 923
      |||||  ||||  ||||  ||||  ||||  ||||  ||||  ||||  ||||  |||||
Db      687 CGGAGGCTGTGGGAGGACCACTTTCATTTGCTGTCTCTTCTCTCTCTCTG 746
      |||||  ||||  ||||  ||||  ||||  ||||  ||||  ||||  ||||  |||||
Qy      924 CGGCAATTCCTGCTCAGGTTTGTGCAATTAAGTACAAAGAACACACCGCCAGAACACTT 983
      |||||  ||||  ||||  ||||  ||||  ||||  ||||  ||||  ||||  |||||
Db      747 TGGCAATTTTGGGATCGGCTTTGGCCCTGAAGTCAAGACACATCGCAAAAACACTT 806
      |||||  ||||  ||||  ||||  ||||  ||||  ||||  ||||  ||||  |||||
Qy      984 TGAGAAAGCAAGAACCCCGGCTGCAACCTCATTCAGTGTGGCGGTAGTTACGAGC 1043
      |||||  ||||  ||||  ||||  ||||  ||||  ||||  ||||  ||||  |||||
Db      807 TGAGAAAGCGGGAACCCCTGCGGAGGTGTGATTCAGTCTGCTGGAGATTTCTATGCTAC 866
      |||||  ||||  ||||  ||||  ||||  ||||  ||||  ||||  ||||  |||||
Qy      1044 TGA 1046
      |||||  ||||  ||||  ||||  ||||  ||||  ||||  ||||  ||||  |||||
Db      867 TAA 869

RESULT 13
US-10-128-870-17
; Sequence 17, Application US/10128870
; Patent No. US20020168724A1
; GENERAL INFORMATION:
; APPLICANT: Blonar, Michael A.
; APPLICANT: Dworetzky, Steven
; APPLICANT: Gribkoff, Valentin K.
; APPLICANT: Levesque, Paul C.
; APPLICANT: Little, Wayne A.
; APPLICANT: Neubauer, Michael G.
; APPLICANT: Yang, Wen-Pin
; TITLE OF INVENTION: KCNO POTASSIUM CHANNELS AND METHODS OF MODULATING SAME
; FILE REFERENCE: DC38ADIV
; CURRENT APPLICATION NUMBER: US/10/128,870
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 09/105,058
; PRIOR FILING DATE: June 26, 1998
; PRIOR APPLICATION NUMBER: 60/055,599
; PRIOR FILING DATE: August 12, 1997
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 930
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: 930 nucleotides of human KCNO3
US-10-128-870-17

Query Match      13.6%; Score 363.8; DB 9; Length 930;
Best Local Similarity 65.5%; Pred. No. 4,1e-97;
Matches 580; Conservative 0; Mismatches 272; Indels 33; Gaps 2;

Qy      186 GAGTACCCAGAGCTGGCGGGGCAACGTCAGTACCGCGGGGTGAGAGTACCTGTACAA 245
      |||||  ||||  ||||  ||||  ||||  ||||  ||||  ||||  ||||  |||||
Db      12 GAGCGCCCGGAGTCAAGAAAGAACACGCGGAGTACCGGGCATCAAACTTTGATCTAGGA 71
      |||||  ||||  ||||  ||||  ||||  ||||  ||||  ||||  ||||  |||||
Qy      246 CGTGTGAGAGAGACCCCGGGCTGGGGCTTCATCTACACGCTTTGCTTCTCTCTTGT 305
      |||||  ||||  ||||  ||||  ||||  ||||  ||||  ||||  ||||  |||||
Db      72 CCCCCGAGAGACCCCGGGCTGGGGCTTCATCTACACGCTTTGCTTCTCTCTTGT 131
      |||||  ||||  ||||  ||||  ||||  ||||  ||||  ||||  ||||  |||||
Qy      306 CTTTGGTCTGCTGATTTTGTCACTGTTTCTACCATCCCGAGAGACACMAAATTTGGCTC 365
      |||||  ||||  ||||  ||||  ||||  ||||  ||||  ||||  ||||  |||||
Db      132 CCGGGGCTGTGATTTGCTGCTCTCCGACCAATTCAGAGATATAGAGACTGTCTGGG 191
      |||||  ||||  ||||  ||||  ||||  ||||  ||||  ||||  ||||  |||||
Qy      366 AAGTGGCTCTTGATCTCGTGAAGTTTGTGATGATGCTCTTTGGTGTGAGTTCATCAT 425
      |||||  ||||  ||||  ||||  ||||  ||||  ||||  ||||  ||||  |||||
Db      192 AGACTGGCTCTTCTTACTGAGACATTTGCTATTTTTCATCTTTGGAGCCGAGTTTGCCTT 251
      |||||  ||||  ||||  ||||  ||||  ||||  ||||  ||||  ||||  |||||
Qy      426 TCGAATCTGCTCGCGGTTCTGTTGTGCATATATAGAGATGCAAGAGACTGAGGTT 485
      |||||  ||||  ||||  ||||  ||||  ||||  ||||  ||||  ||||  |||||
Db      252 GAGGATCTGGGCTGTGATGTTGCTGCCATACAAAGGCTGGCGGCCGACCTGAAGCTT 311
      |||||  ||||  ||||  ||||  ||||  ||||  ||||  ||||  ||||  |||||

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Qy      486 TGTGGAAGGCCCTTCTGTGTATAGATACATTTGTTCTTATCGTTCAATAGCACTGTG 545
      |||||  ||||  ||||  ||||  ||||  ||||  ||||  ||||  ||||  |||||
Db      312 TGCCAGGAAGCCCTTGTGATGTGTGACATCTTTTGTGTGATGTGCTGTGTGCACTGGT 371
      |||||  ||||  ||||  ||||  ||||  ||||  ||||  ||||  ||||  |||||
Qy      546 TTTCTCAAAAACCTCAGGTAATATTTTGGCCAGTCTGCACAGAGTCTCCGTTCTT 605
      |||||  ||||  ||||  ||||  ||||  ||||  ||||  ||||  ||||  |||||
Db      372 TGTCTGTGGGAACCAAGGCAATGTTCTGTGCCACT---CCGTGCCAAGGCTGTGGCTTCC 428
      |||||  ||||  ||||  ||||  ||||  ||||  ||||  ||||  ||||  |||||
Qy      606 ACAGATCTCCGCAATGTGCGCATGAGACCGAAGGGAGGCACTTGGAAATTTACTGGTTTC 665
      |||||  ||||  ||||  ||||  ||||  ||||  ||||  ||||  ||||  |||||
Db      429 GCAGATCTCCGCAATGTGCGCATGAGACCGAAGGAGGTGACACTGTGCAACTTCTGTGGCTC 488
      |||||  ||||  ||||  ||||  ||||  ||||  ||||  ||||  ||||  |||||
Qy      666 AGTGTATATGCTCAGACAGCAAGCAATTAATACAGCTTGTGTCATATGAAATTTTGTGTTCT 725
      |||||  ||||  ||||  ||||  ||||  ||||  ||||  ||||  ||||  |||||
Db      489 AGCCATCTGTGCCACAGCAAGCAATCTATACAGGCTGTGTGATGTTTCTGTGACACT 548
      |||||  ||||  ||||  ||||  ||||  ||||  ||||  ||||  ||||  |||||
Qy      726 TATTTTTCGTTCTCTATCTATCTGTGGAAGAGATGCC----- 768
      |||||  ||||  ||||  ||||  ||||  ||||  ||||  ||||  ||||  |||||
Db      549 CATCTTCTTCTATTTCTTGTCTACCTGTGTGGAAGAGAGTCCAGAGGTGATGCACA 608
      |||||  ||||  ||||  ||||  ||||  ||||  ||||  ||||  ||||  |||||
Qy      769 -----AATAAGATTTTCTATATATGCAATGCTCTGTGTGGGCAAT 815
      |||||  ||||  ||||  ||||  ||||  ||||  ||||  ||||  ||||  |||||
Db      609 AGGAGAGGAGATGAAGAGAGAGATTGAGACATATGCAAGATGCCCTGTGTGGGCGCTGAT 668
      |||||  ||||  ||||  ||||  ||||  ||||  ||||  ||||  ||||  |||||
Qy      816 TACATTCACACTATTTGCTATGAGACAAACTCCCTTAAGTGTGCTGGAGATTTGCT 875
      |||||  ||||  ||||  ||||  ||||  ||||  ||||  ||||  ||||  |||||
Db      669 CACACTGCCACCATTTGCTATGAGACAAACCCCAAGTGTGGAAAGGCCGTGAT 728
      |||||  ||||  ||||  ||||  ||||  ||||  ||||  ||||  ||||  |||||
Qy      876 TTTCTCAGGCTTTGACATCTTGTGCAATTTCTTTCTTTGCACTCTCGCGCATTTCTGG 935
      |||||  ||||  ||||  ||||  ||||  ||||  ||||  ||||  ||||  |||||
Db      729 TGCGGCAACCTTTCTTCTTAATTTGGGCTCTCTTTTGTGCGCTTCAAGCGGCGATTCGTGG 788
      |||||  ||||  ||||  ||||  ||||  ||||  ||||  ||||  ||||  |||||
Qy      936 CTCAGATTTTGCATTAAAGTACAGACACACACCGCCGCAAACTTTAGAGAAAGAG 995
      |||||  ||||  ||||  ||||  ||||  ||||  ||||  ||||  ||||  |||||
Db      789 GTCCGGCGCTGGCCCTCAAGGTGAGAGACACACCGCTCAAGAACTTTGAGAAAGAGAG 848
      |||||  ||||  ||||  ||||  ||||  ||||  ||||  ||||  ||||  |||||
Qy      996 GAACCCAGCTGCCAAGCTCATTCAGTGTGTTGGCGCTAGTACGC 1040
      |||||  ||||  ||||  ||||  ||||  ||||  ||||  ||||  ||||  |||||
Db      849 GAAGCCAGCTGCTGAGCTATTTCAGGCTGCTGTGAGATTAATG 893
      |||||  ||||  ||||  ||||  ||||  ||||  ||||  ||||  ||||  |||||

RESULT 14
US-10-128-870-7
; Sequence 7, Application US/10128870
; Patent No. US20020168724A1
; GENERAL INFORMATION:
; APPLICANT: Blonar, Michael A.
; APPLICANT: Dworetzky, Steven
; APPLICANT: Gribkoff, Valentin K.
; APPLICANT: Levesque, Paul C.
; APPLICANT: Little, Wayne A.
; APPLICANT: Neubauer, Michael G.
; APPLICANT: Yang, Wen-Pin
; TITLE OF INVENTION: KCNO POTASSIUM CHANNELS AND METHODS OF MODULATING SAME
; FILE REFERENCE: DC38ADIV
; CURRENT APPLICATION NUMBER: US/10/128,870
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 09/105,058
; PRIOR FILING DATE: June 26, 1998
; PRIOR APPLICATION NUMBER: 60/055,599
; PRIOR FILING DATE: August 12, 1997
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 735
; TYPE: DNA
; ORGANISM: RAT
US-10-128-870-7

Query Match      12.5%; Score 334.2; DB 9; Length 735;
Best Local Similarity 68.4%; Pred. No. 1,9e-88;
Matches 462; Conservative 0; Mismatches 213; Indels 0; Gaps 0;

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QY 372 CCTGTGATCCCTGAGAGTTCGTGATGATTCGCTTGTGGAGTTGATCATTCGAAAT 431
    ||||| ||| ||||| ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 30 CCTGTGATCCCTGAGAGTTCGTGATGATTCGCTTGTGGAGTTGATCATTCGAAAT 89
QY 432 CTGCTGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 491
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 90 CTGCTGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 149
QY 492 AAAAGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 551
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 150 GAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 209
QY 552 AAAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 611
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 210 TGGCTCCAGGAGCATGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 269
QY 612 CCTCCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 671
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 270 CTTCAGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 329
QY 672 TTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 731
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 330 CTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 389
QY 732 TTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 791
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 390 GGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 449
QY 792 AGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 851
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 450 GGAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 509
QY 852 CCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 911
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 510 TCGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 569
QY 912 TGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 971
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 570 CGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 629
QY 972 CGAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1031
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 630 GCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 689
QY 1032 TAGTACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1046
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 690 ATTCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 704

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; NAME/KEY: CDS
; LOCATION: (1)..(2028)
US-09-840-125-1
Query Match 10.0%; Score 267.8; DB 10; Length 2028;
Best Local Similarity 59.5%; Pred. No. 1.7e-68;
Matches 499; Conservative 0; Mismatches 322; Indels 18; Gaps 2;

QY 226 GTGACAGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 282
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Db 316 GTCCAGAGGCGCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 375
QY 283 CAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 342
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 376 CACTTCCGCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 435
QY 343 CTTGAGCAGCAAAATTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 402
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 436 GAGCAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 495
QY 403 GTCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 462
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 496 TTCTTGGGAGCGAGTACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 555
QY 463 GATGCGCAGCAAAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 522
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 556 GGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 615
QY 523 CTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 582
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 616 GTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 675
QY 583 GCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 642
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 676 GCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 735
QY 643 GGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 702
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 736 GGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 795
QY 703 TGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 762
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 796 CTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 855
QY 763 GATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 807
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 856 GAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 915
QY 808 GGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 867
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 916 GGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 975
QY 868 AGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 927
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 976 AAGACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1035
QY 928 ATTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 987
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Db 1036 ATTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1095
QY 988 AAAAGAGGAGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1046
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1096 CGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1154

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Search completed: January 11, 2003, 18:00:41
 Job time : 108 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: January 11, 2003, 17:21:17 ; Search time 3948 Seconds
(without alignments)
6545.920 Million cell updates/sec

Title: US-09-810-796-5
Perfect score: 4347
Sequence: 1 MKDVEGSRGRVLLNSAARG.....SICKAGESTDLSPHYKXK 888

Scoring table:
BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2054640 seqs, 14551402878 residues
Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-Q/cg92.1/USFTO.spool/US0810796/runal.10012003.085456.22806/app_query.fasta-1.1031
-DB-GenEmbl -OFMT=fasta -SUFFIX=p2n.rge -MINMATCH=0.1 -LOOPEXT=0 -LIST=45
-UNITS-bits -START=1 -END=1 -MATRIX-blosum62 -TRANS-human40.cdi -MODE=LOCAL
-DOCALLIGN=200 -THR_SCORE=pcr -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
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-YGAPOP=10 -YGAPEXT=0.5 -DELop=6 -DELEXT=7

Database : GenEmbl:*
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2: gb_htg:*
3: gb_in:*
4: gb_lm:*
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pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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4	4527.5	99.6	3137	6 AX056817	AX056817 Sequence
5	4527.5	99.6	3137	6 AF202977	AF202977 Homo sapi
6	4513.5	99.3	3074	6 AX253254	AX253254 Sequence
7	4513.5	99.3	3074	6 AX456864	AX456864 Sequence
8	4513.5	95.2	3074	6 AF249278	AF249278 Homo sapi
9	4328.5	93.0	2832	6 AF263835	AF263835 Homo sapi
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11	2007.5	44.1	2335	6 AX032994	AX032994 Sequence
12	2007.5	44.1	2335	6 AX456863	AX456863 Sequence
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14	1810	39.8	4165	10 AF087453	AF087453 Rattus no
15	1804.5	39.7	2613	10 AF490773	AF490773 Mus muscu
16	1797	39.5	7420	9 HSKCND2	AF074247 Homo sapi
17	1790	39.4	2565	6 AF074247	AF074247 Mus muscu
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RESULT 1

ALIGNMENTS

AX268474
LOCUS AX268474 2772 bp DNA linear PAT 29-OCT-2001
DEFINITION Sequence 1 from Patent WO0175108.
ACCESSION AX268474
VERSION AX268474.1 GI:16541652
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
REFERENCE
AUTHORS Hu, Y., Kieke, J. A., Turner, A. C., Nehls, M. C., Friedrich, G. B.,
Zambowicz, B. and Sands, A. T.
TITLE Human ion channel protein and polynucleotides encoding the same
JOURNAL Patent: WO 01/5108-A 1 11-OCT-2001;
Lexicon Genetics Incorporated (US)
FEATURES
source 1.2772
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 715 a 700 c 713 g 644 t
ORIGIN

Alignment Scores:
Pred. No.: 1.97e-312 Length: 2772
Score: 4547.00 Matches: 888
Percent Similarity: 100.00% Conservative: 0
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US-09-810-796-5 (1-888) x AX268474 (1-2772)

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DEFINITION Sequence 3 from Patent WO0175108.
ACCESSION AX268476
VERSION AX268476.1 GI:16541653

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KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
REFERENCE
AUTHORS Hu, Y., Kieke, J. A., Turner, A. C., Nehls, M. C., Friedrich, G. B.,
Zambrowicz, B., and Sands, A. T.
TITLE Human ion channel protein and polynucleotides encoding the same
JOURNAL Patent: WO 0175108-A 3 11-OCT-2001.
Lexicon Genetics Incorporated (US)
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REFERENCE 1
AUTHORS Dworetzky,S.I., Ramanathan,C.S., Trojnecki,J.T., Boissard,C.G. and
Gibkoiff,V.R.
TITLE Human Kcnq3 potassium channel, methods and compositions thereof
JOURNAL Patent: WO 0192526-A 1 06-DEC-2001;
Bristol-Myers Squibb Company (US)
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DEFINITION AX056817
ACCESSION AX056817
VERSION AX056817.1 GI:12309758
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SOURCE human.
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REFERENCE 1 (bases 1 to 3137)
AUTHORS Jensch, T.U.
TITLE Novel potassium channels and genes encoding these potassium
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JOURNAL Patent: WO 0077035-A 1 21-DEC-2000;

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 Schroeder,B.C., Hechenberger,M., Weinreich,F., Kubisch,C. and Jentsch,T.J.
 KCNQ5, a novel potassium channel broadly expressed in brain, mediates M-type currents
 J. Biol. Chem. 275 (31), 24089-24095 (2000)
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 Schroeder,B.C., Hechenberger,M., Weinreich,F., Kubisch,C. and Jentsch,T.J.
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LOCUS AX253254
DEFINITION Sequence 1 from Patent WO01/0811.
ACCESSION AX253254
VERSION AX253254.1 GI:16073802
KEYWORDS
SOURCE human.
ORGANISM Homo Sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 3074)
AUTHORS Lerche,C., Scherer,C., Seebom,G., Busch,H. and Steinmeyer,K.
TITLE potassium channel protein kno5, a target for diseases of central
nervous system and cardiovascular system
JOURNAL Patent: WO 01/0811-A I 27-SEP-2001;
Aventis Pharma Deutschland GmbH (DE)
FEATURES
source location/Qualifiers
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Percent Similarity: 98.77% conservative: 1
Best Local Similarity: 98.66% mismatches: 2
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Db 275 GACGGCTGCTACTGCTGGGACCCGCGGCGCACGCTTGTGTGGCGGCGGTGCGCTG 334

OY	41	ArgGIuSerArGArGlyLysSgInGlyAlaArgMetSerLeuLeuGIlySProLeuSer	60
Db	335	ACGGAGAGCGCGGGGCAAGCAGGGGGCCGGATGAGCCTGCTGGGAACCGCCCTCTCT	394
OY	61	TyrThrSerSerGIuSerCysArGArGAsnValLysTyrArGArGValGIuAsnTyrLeu	80
Db	395	TACACAGTAGCCAGAGCTGCGCGGCAACGTCAAGTACCGGGGGGGCGAAGCTACTCG	454
OY	81	TyrAsnValLeuGIuArGProArGlyTyrPalAPheIleTyrHisAlaPheValPheLeu	100
Db	455	TCAACAGTCTGGAGAGACCCCGGCTGGGCTCATCTACACAGGCTTCGTTTTCCCTC	514
OY	101	LeuValPheGIyCysLeuIleLeuSerValPheSerThrIleProGIuHisThrLysLeu	120
Db	515	CTTGCTTTGGTGGCTTGATTTTGTGAGTGTTCACCATTCCTCCAGGCAACAAAATTG	574
OY	121	AlaSerSerCysLeuLeuIleLeuGIuPheValMetIleValValPheGIyLeuGIuPhe	140
Db	575	GCCTCAGTGGCTCTTGATCCTCGGAGTTCGTATGATGTGCTGCTTTGGTTGGACTTC	634
OY	141	IleIleArGIleTyrSerAlaGIyCysCysArGIyTyrArGIyTyrGIuInGIyArGIu	160
Db	635	ATCATTCGATCTGGCTCGCGGGTCTGTTGTCGATATAGAGATGGCAAGAGACGCTG	694
OY	161	ArgPheAlaArGIySProPheCysValIleAspThrIleValLeuIleAlaSerIleAla	180
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OY	201	PheLeuGIuIleLeuArGIyMetValArGIyMetAspArGIyGIyThrTyrLysLeuLeu	220
Db	815	TTCCATACAGATCCTCGCATGTGGCGCATGAGACCGAAGGGAGGACCTTGAAATTAATCTG	874
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Db	875	GGTTCAGTGGTTATAGCTCACAGCAAGAAATTAATCAACAGCTTGATACATAGGATTTTGG	934
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Db	995	TCATACATGACAGATCTCTGCTGGGGACAAATTACATGACAACTATTTGGCTATGCA	1054
OY	281	AspLysThrProLeuThrThrPheLeuGIyArGIyLeuLeuSerAlaGIyPheAlaLeuLeuGIy	300
Db	1055	GACAAAAACCCCTTAACCTTGGCGGAGAAATTCCTTTCGACAGCTTGGACCTCTGGCG	1114
OY	301	IleSerPhePheAlaLeuProAlaGIyIleLeuGIySerGIyPheAlaLeuLysValGIu	320
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OY	321	GIuGIuHisArGIuLysHisPheGIuLysArGIyAsnProAlaIleAsnLeuIleGIu	340
Db	1175	GAACAACACCGCCAGAAACACTTTGAGAAAAGAGAACACCAGCTGCCAACCTCATTTACG	1234
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OY	392	LysSerArGIuAlaSerValGIySAspArGIySerProSerThrAspIleThrAlaGIu	411
Db	1415	AAGAGCCGACAAAGCCTAGTAGGAGACAGGAGTCCCAACACAGCATACAGCCGAG	1474
OY	412	GIySerProThrLysValGIuLysSerTyrSerPheAsnAspArGIyThrArgPheArgPro	431
Db	1475	GGCAGTCCCAACAAAGTGCAGAGAGCTGGAGCTTCAACAGCCAGACCCGCTTCGGGCC	1534
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OY	452	ThrAspAspValTyrAspGIuLysGIyCysGIuLysAspValSerValGIuAspLeuThr	471
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OY	472	ProProLeuLysThrValIleArGIuAlaGIyIleArGIuIleMetLysPheHisValAlaLysArG	491
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Db	1835	GGAAGAGGCAATACATCATCAGATACAGAGCCGAGAGAAATTAACAGCAAGACATGAG	1894
OY	552	ThrThrAspAspLeuSerMetLeuGIyArGIyValValLysValGIuLysGIuValGIuSer	571
Db	1895	ACCACAGACCATCTCAGTATGCTCGTGGGTGCTCAAGGTGTGAAGAAACAGGTACAGTCC	1954
OY	572	IleGIuSerLysLeuAspCysLeuLeuAspIleTyrGIuGIuInValLeuArGIyGIySer	591
Db	1955	ATAGAATCCAGGCTGCACTGCTACTGACACTCATATCAACAGGTCCTTGGAAAGGCTCT	2014
OY	592	AlaSerAlaLeuAlaLeuAlaSerPheGIuIleProProPheGIuCysGIuGIuThrSer	611
Db	2015	GCCACAGCCCTCGCTTTGGCTTCAATTCAGATCCACCTTTTGATGTGAAGACAGCATCT	2074
OY	612	AspTyrGIuInSerProValAspSerLysAspLeuSerGIySerAlaGIuAsnSerGIyCys	631
Db	2075	GACTATCAAAAGCCCTGTGATAGCAAGATCTTTCGGGTTCCGCACAAAACAGTGGCTGC	2134
OY	632	LeuSerArGIySerThrSerAlaAsnIleSerArGIyLeuGIuPheIleLeuThrProAsn	651
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ACCESSION AX456864
VERSION AX456864.1 GI:21715731
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REFERENCE 1
AUTHORS Argenteier, T.M. and Sheldon, J.H.
TITLE Methods of selecting compounds for modulation of bladder function
JOURNAL Patent: WO 0232960-A 5 25-APR-2002;
METHODS myeth (us)
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US-09-810-796-5 (1-888) x AX456864 (1-3074)

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 Lerche,C., Scherer,C.R., Seebom,G., Derst,C., Wei,A.D., Busch,A.E.
 and Steinmeyer,K.
 Molecular cloning and functional expression of KCNQ5, a potassium
 channel subunit that may contribute to neuronal M-current diversity
 J. Biol. Chem. 275 (29), 22395-22400 (2000)
 PUBMED
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 Lerche,C., Scherer,C.R., Seebom,G., Derst,C., Wei,A.D., Busch,A.E.
 and Steinmeyer,K.
 Direct Submission
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REFERENCE 1 (bases 1 to 2832)
AUTHORS Kniazeva,M. and Han,M.
TITLE A new gene of the voltage-gated potassium channel KCNQ family,
KCNQ5, is a candidate gene for retinal disorders
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 2832)
AUTHORS Kniazeva,M. and Han,M.
TITLE Direct Submission
JOURNAL Submitted (04-MAY-2000) MCB, University of Colorado at Boulder,
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2401 ACTGATGAAGAGGTGGTCCCGCAGAGACAGACAGACACTTTTATGCCGACCGCAGAC 2460
QY 848 ProAlaArgGlnAlaAlaPheAlaSerAspSerLeuArgThrGlyArgSerArgSerSer 867
2461 CCTGCGCAGGAAAGCTGCTTTCATCTCAGACTCTTAAGACACTGGAAGGTGCACAAATCATCT 2520
QY 868 GlnSer1IleCysLysAlaGlyGlnSerThrAspAlaLeuSerLeuProHisValLysLeu 887
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QY 888 Lys 888
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db 2561 AAA 2583

RESULT 10

LOCUS AF263836 3108 bp mRNA linear ROD 01-JUN-2000

DEFINITION Mus musculus voltage-gated potassium channel KCNQ5 (Kcnq5) mRNA,

ACCESSION AF263836

VERSION AF263836

KEYWORDS partial cds.

SOURCE Mus musculus.

ORGANISM Mus musculus.

REFERENCE 1 (bases 1 to 3108) Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

AUTHORS Kniazeva, M. and Han, M.

TITLE A new gene of the voltage-gated potassium channel KCNQ family..

JOURNAL KCNQ5 is a candidate gene for retinal disorders

REFERENCE Unpublished

AUTHORS 2 (bases 1 to 3108)

TITLE Kniazeva, M. and Han, M.

JOURNAL Direct Submission

Submitted (04-MAY-2000) MCDB, University of Colorado at Boulder, Porter Biosciences Bldg., Boulder, CO 80309, USA

FEATURES

source

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BASE COUNT 830 a 779 c 748 g 743 t 8 others

ORIGIN

Alignment Scores:

Pred. No.: 9,86e-290 Length: 3108

Score: 4227.50 Matches: 827

Percent Similarity: 95.90% Conservative: 14

Best Local Similarity: 94.30% Mismatches: 27

Query Match: 92.97% Indels: 9

Gaps: 1

US-09-810-796-5 (1-888) x AF263836 (1-3108)

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QY	60	SerTyrThrSerSerClnSerCysAgaIAsnValLysTyrTrpArgValLgIAsnTyr	79
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QY	80	LeuTyrAsnValLeuLurArgProArgIlyTPalAphLeuTyrHisAlaPheValPhe	99
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QY	120	LeuAlaSerSerCysLeuLeuIleLeuGluPheValMetLleValValPheGlyLeuGlu	139
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 VERSION AX032994.1 GI:10279897
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 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE
 AUTHORS Jentsch,T.J.
 TITLE Novel potassium channels and genes encoding these potassium
 channels
 JOURNAL Patent: WO 0044786-A 1 03-Aug-2000;
 NEUROSEARCH AS (DK)
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Percent Similarity: 65.32%
 Best Local Similarity: 54.94%
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US-09-810-796-5 (1-888) x AX032994 (1-2335)

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 Oy 352 rValSerIleAlaThrTrp----- 358
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 Oy 358 ----- 358
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RESULT 15
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LOCUS AF490773 Mus musculus potassium channel KCNQ2 mRNA, complete cds.
DEFINITION AF490773 AF490773.1 GI:20069140
VERSION AF490773.1 GI:20069140
KEYWORDS
SOURCE Mus musculus.
ORGANISM Mus musculus.
MUS musculus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
1 (bases 1 to 2613)
Wen, H. and Levitan, I. B.
Calmmodulin is an auxiliary subunit of KCNQ channels
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 2613)
Wen, H. and Levitan, I. B.
Direct Submission
TITLE Submitted (07-MAR-2002) Neuroscience, University of Pennsylvania,
JOURNAL 3450 Hamilton Walk, Philadelphia, PA 19104, USA

FEATURES
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BASE COUNT 553 a 770 c 766 g 524 t

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QY 642 ArgGly-----LeuGlnPheIleLeuThrProAsnGlu 652
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QY 653 PheSerAlaGlnThrPheThrAlaLeuSerProThrMet-----HisSer 667
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QY 668 GlnAlaThrGlnValProIleSerGlnSerAspGly-----SerAlaValAlaAlaThr 685
Db 2213 TACGCATCCACACACCCCTGCACACAGCGGTGCTGTGCTTACGCTGGGGGCAACA 2272
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Search completed: January 11, 2003, 19:13:06
Job time : 4019 secs

GenCore version 5.1.3
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OM protein - nucleic search, using frame_plus.p2n model

Run on: January 11, 2003, 16:04:17 ; Search time 298 Seconds
(without alignments)
6710.653 Million cell updates/sec

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Perfect score: 4547
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Scoring table:
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Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2185239 segs, 112599159 residues
Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
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Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4547	100.0	2667	AA514653	Human cDNA encoding
2	4547	100.0	2772	AAH43633	Human ion-channel
3	4547	100.0	3111	AAH43634	Human ion-channel
4	4527.5	99.6	2694	AA514652	Human cDNA encoding
5	4527.5	99.6	2694	AA514652	Human cDNA encoding
6	4527.5	99.6	3137	AA514651	Human cDNA for vol
7	4523.5	99.5	3071	AA514651	Human cDNA for vol
8	4513.5	99.3	3074	AA514651	Human cDNA for vol
9	4346.5	95.6	3718	AA514651	Human cDNA for vol
10	2007.5	44.1	2335	AA514651	Human cDNA for vol
11	1794	39.5	3237	AA514651	Human cDNA for vol
12	1792.5	39.4	3287	AA514651	Human cDNA for vol
13	1790.5	39.4	2169	AA514651	Human cDNA for vol
14	1790	39.4	2565	AA514651	Human cDNA for vol
15	1790	39.4	3195	AA514651	Human cDNA for vol
16	1788	39.3	3232	AA514651	Human cDNA for vol
17	1780	39.1	3232	AA514651	Human cDNA for vol
18	1775	39.0	7413	AA514651	Human cDNA for vol
19	1767	38.9	2273	AA514651	Human cDNA for vol
20	1762	38.8	3029	AA514651	Human cDNA for vol
21	1667.5	36.7	125910	AA514651	Human cDNA for vol
22	1587.5	34.9	2565	AA514651	Human cDNA for vol
23	1587.5	34.9	2914	AA514651	Human cDNA for vol
24	1550.5	34.1	2814	AA514651	Human cDNA for vol
25	1446.5	31.8	2901	AA514651	Human cDNA for vol
26	1439.5	31.7	2911	AA514651	Human cDNA for vol
27	1439.5	31.7	4154	AA514651	Human cDNA for vol
28	1248	27.4	3335	AA514651	Human cDNA for vol
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30	1226.5	27.0	1425	AA514651	Human cDNA for vol
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45	933.5	20.5	1566	AA514651	Human cDNA for vol

ALIGNMENTS

RESULT 1
AA514653 standard; cDNA; 2667 BP.

AC AA514653:
DT 18-DEC-2001 (first entry)

DE Human cDNA encoding a voltage gated potassium channel hKv9.2.

XX Human; ss; voltage-gated potassium channel; KCNQ5-2; nocitropic;
XX cerebropotective; neurotropic; analgesic; vision disorder;
XX central nervous system disorder; epilepsy; migraine; hearing disorder;
XX psychotic disorder; seizure; learning disorder; memory disorder;
XX stroke; pain; gene therapy; splice variant.

XX Homo sapiens.
XX

FH Key Location/Qualifiers
 FT 1..2967
 FT CDS /tag= a
 FT /product= "hKCNQ5-2"
 PN WO200170759-A1.
 PN XX
 PD 27-SEP-2001.
 PD XX
 PE 20-MAR-2001; 2001WO-US09328.
 PE XX
 PR 21-MAR-2000; 2000US-190954P.
 PR XX
 PA (ICAG-) ICAGEN INC.
 PA XX
 PI Jega1a TJ;
 PI XX
 DR WP1; 2001-611467/70.
 DR XX
 DR P-PSDB; AAU09021.
 DR XX
 PT Polypeptides and polynucleotides of potassium channel KCNQ5 for
 PT identifying a compound modulating ion flux in eukaryotic cell or cell
 PT membrane expressing the protein, comprises KCNQ alpha
 PT subunits
 PT XX
 PS Claim 5; Page 63-64; 78pp; English.
 PS XX
 CC The invention relates to an isolated polypeptide comprising an
 CC alpha subunit of a KCNQ potassium channel, with a subsequence having
 CC 65% sequence identity to amino acids 343-640 of hKCNQ5-1 amino acid
 CC sequence and forms a KCNQ potassium channel having the characteristic of
 CC voltage-gating with at least an additional KCNQ alpha-subunit. Also
 CC included in the scope of the invention are the nucleic acids encoding
 CC hKCNQ5 (including splice variants encoding hKCNQ5-1 and hKCNQ5-2),
 CC expression vectors encoding them, antibodies against them, the use of
 CC 3-dimensional computer modelling to identify molecules that bind to a
 CC KCNQ containing potassium channel and modulate ion flux through the
 CC channel. The KCNQ polypeptide is useful for identifying a compound that
 CC increases or decreases ion flux through a potassium channel expressed in
 CC an eukaryotic host cell or cell membrane. The compound (and the
 CC KCNQ nucleic acid when used in gene therapy) is useful as
 CC a pharmaceutical agent for treating diseases involving abnormal ion flux,
 CC such as disorders of the central nervous system, such as epilepsy,
 CC migraines, hearing and vision problems, psychotic disorders, seizures,
 CC learning and memory disorders, stroke and pain. The antibodies are
 CC useful for detecting a KCNQ5 polypeptide in a human tissue and the
 CC use of a nucleotide sequence of KCNQ5 to search computer databases to
 CC find variants of the sequence which are associated with disease states,
 CC is useful for screening mutations of KCNQ5. The present sequence is
 CC a splice variant of hKCNQ5 encoding hKCNQ5-2.
 CC XX
 SQ Sequence 2667 BP; 701 A; 667 C; 660 G; 639 T; 0 other;
 SQ XX
 Alignment Scores:
 Pred. No.: 0 Length: 2667
 Score: 4547.00 Matches: 888
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 22 Gaps: 0
 US-09-810-796-5 (1-888) x AAS14653 (1-2667)
 QY 1 MetLysAspValGluSerGlyArgGlyArgValLeuLeuAsnSerAlaAlaAlaArgGly 20
 DB 1 ATGAAGATGTGAGTGGGCGCGGCGAGAGGTGCTGCTGAACCTGGCGACGCCAGGAGG 60
 QY 21 AspGlyLeuLeuLeuLeuGlyThrArgAlaAlaThrLeuGlyGlyGlyGlyGlyLeu 40
 DB 61 GACGGCTGCTACTGCTGGGCGACCCGCGCGCCACGCTGTGGGCGGCGGCGGTGGCTG 120
 QY 41 ArgGluSerArgArgGlyGlyGlyGlyAlaArgMetSerLeuLeuGlyLysProLeuSer 60
 DB 1201 AGGAGTCCCAAGCACCAGCATCACAGCCGAGGCGCAGTCCCAAGAGTGCAGAAAGAGC 1260

DB 121 AGGAGAGCCCGCGGCGAAGCAGGCGCCCGGATGACCTGCTGGGAGCCGCTCTCT 180
 QY 61 TyrThrSerSerGlnSerGlyArgArgAsnValLysTyrArgArgValGlnAsnTyrLeu 80
 DB 181 TACACAGATACCCAGAGAGCTGCGGCGCAAGCTCAAGTACCGCGGGTGCAGACACTACCTG 240
 QY 81 TyrAsnValLeuGluArgProArgGlyTyrPalapheLleTyrHisAlaPheValPheLeu 100
 DB 241 TACACAGTGTGAGAGAACCCCGCGGCGGTTCATCATCACACGCTTGTGTTTCTC 300
 QY 101 LeuValPheGlyCysLeuLleLeuSerValPheSerThrIleProGlnHisThrLysLeu 120
 DB 301 CTGTCCTTGGTGGTCTGATTTTGTACAGTGTTCCTACCATCCTCGACACACAAATTTG 360
 QY 121 AlaSerSerCysLeuLeuLleLeuGluPheValMetIleValValPheGlyLeuGluPhe 140
 DB 361 GCCTCAGTGGCTCTTGATCCTGAGCTGAGTGTGATGATTCGTCCTTGGTTGGAGTTC 420
 QY 141 IleLeuArgIleTyrSerAlaGlyCysCysArgTyrArgGlyTyrPGLnglyArgLeu 160
 DB 421 ATCATTCGAATCTGCTGCGGGGTTCGTTGTGATATAGAGATGCGCAAGAAAGACTG 480
 QY 161 ArgPheAlaArgLysProPheCysValIleAspThrIleValLleuLleAlaSerIleAla 180
 DB 481 AGGTTTCTCGAAAGCCCTTCTGTATATACATACCATGTTCTTATCGCTTCAATFACA 540
 QY 181 ValValSerAlaLysThrGlnGlyAsnIlePheAlaThrSerAlaLeuArgSerLeuArg 200
 DB 541 GTTGTCTTCGAAAACTCAGGAGTAATATTTTCCACGCTGCACAGCAAGTCCGCT 600
 QY 201 PheLeuGlnIleLeuArgMetValArgMetAspArgArgGlyGlyThrTrpLysLeuLeu 220
 DB 601 TTCCTACAGATCCCTCGCAAGTGGCATGACCGAAGGAGGACACTGGAATTTACTG 660
 QY 221 GlySerValValTyrAlaHisSerLysGluLeuLleThrAlaTyrPylIleGlyPheLeu 240
 DB 661 GGTTACAGTGGTTATAGTGTACAGCAAGAAATTAATCACAGCTTGTGTCATAGATTG 720
 QY 241 ValLeuIlePheSerSerPheLeuValTyrLeuValGluLysAspAlaAsnLysGluPhe 260
 DB 721 GTTCTATATTTTTCGTTCTTCTGCTATCTGTTGGAAGAGTGCATTAAGAGATT 780
 QY 261 SerThrTyrAlaAspAlaLeuTyrTrpGlyTyrThrLeuThrTrpIleGlyTyrGly 280
 DB 781 TCACATATGCAATAGTCTCTGCTGGGCGACAAATTAATTAATTAATTAATTAATTAAT 840
 QY 281 AspLysThrProLeuThrTrpLeuGlyArgLeuLeuSerAlaGlyPheAlaLeuLeuGly 300
 DB 841 GACAAACCTCCCTTAACCTGCTGGGAAGATTGCTTCTGACAGCTTGGCACTCCTTGGC 900
 QY 301 IleSerPhePheAlaLeuProAlaGlyIleLeuGlySerGlyPheAlaLeuLysValGln 320
 DB 901 ATTTCCTTCTTTCACCTCTCTGCGGCAATTCGCTGAGGTTTGGATTAAGTACAA 960
 QY 321 GluGlnHisArgLysHisPheGluLysArgArgAsnProAlaAlaAsnLeuLleGln 340
 DB 961 GAACAACACCGCCAGAAACCTTGAAGAAAGAAAGAACCAAGCTGCAACCTATTTCAG 1020
 QY 341 CysValTyrPheSerTyrAlaAlaAspGluLysSerValSerIleAlaThrTrpLysPro 360
 DB 1021 TGTGTTGGCGTAGTACGAGCTGATGAGAAATTCGTTCCATTGCAACCTGGAACCA 1080
 QY 361 HisLeuLysAlaLeuHisThrCysSerProThrAsnGlnLysLeuSerPheLysGluArg 380
 DB 1081 CACTTAAGGCTTGACACACTGCAAGCTTACCAATTCAGAACTTAAGTTTAAGAGACGA 1140
 QY 381 ValArgMetAlaSerProArgGlyGlnSerIleLysSerArgGlnAlaSerValGlyAsp 400
 DB 1141 GTGGCATGGCAGAGCCGAGGCGCAGAGATTAAGAGCCGCAAGCTCAGTAAGGTGAC 1200
 QY 401 ArgArgSerProSerThrAspIleThrAlaGluGlySerProThrLysValGlnLysSer 420
 DB 1201 AGGAGTCCCAAGCACCAGCATCACAGCCGAGGCGCAGTCCCAAGAGTGCAGAAAGAGC 1260


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QY 101 LeuValPheGlyCysLeuIleLeuSerValPheSerThrIleProGluHisThrLysLeu 120
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Db 465 CTGTGCTTGGTGGCTTAATTTTGTACAGTGTCTTCTACCATCCCTGACACACAAATTTG 524
QY 121 AlaSerSerCysLeuLeuIleLeuGluPheValMetIleValValPheGlyLeuGluPhe 140
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Db 525 GCGCAAGTGCCTCTGATCCTCGATGCGATGATGATGATGATGATGATGATGATGATGATG 584
QY 141 IleIleArgIleIlePheSerAlaGlyCysCysArgGlyArgGlyTrpGlnGlyArgLeu 160
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Db 585 ATCATTCGAATCTGGTCTGCGGGTGTCTGTTCATATATAGAGGATGAGGAGGAGGAGGAGG 644
QY 161 ArgPheIleAlaGlySerProPheCysValIleAspThrIleValLeuIleLeuSerIleAla 180
|||||
Db 645 AGGTTTGCTCGAAGCCCTTCTGTGTATATAGATACCATTTGCTTATCCGCTTCAATAGCA 704
QY 181 ValValSerAlaValThrGlnGlyAsnIlePheAlaThrSerAlaLeuArgSerLeuArg 200
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Db 705 GTTGTTCGCAAAAACACAGGGTAAATATTTTGGCACGCTCGCACTCAGAACTCTCCGT 764
QY 201 PheLeuGlnIleLeuArgMetValArgMetAspArgArgGlyGlyThrTrpLysLeuLeu 220
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Db 765 TTCCTACAGATCTCCGATGGTGGCATGACCGAAGGGAGGACCTGGAAATTAATCTG 824
QY 221 GlySerValValIleValIleHisSerLysGluLeuIleThrAlaTrpTrpIleGlyPheLeu 240
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Db 825 GGTTCAGAGGTTTATAGCTCACAGCAAGAAATTAATCACAGCTTGGTACATAGGATTTTGG 884
QY 241 ValLeuIlePheSerSerPheLeuValIleLeuValGluLysAspAlaAsnLysGluPhe 260
|||||
Db 885 GTTCTATATTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 944
QY 261 SerThrTrpAlaAspAlaLeuTrpTrpGlyThrIleThrLeuThrThrIleGlyTrpGly 280
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Db 945 TCTACATTCGACAGATGCTCTCTGTGGGACACAAATTAATTAATTAATTAATTAATTAAT 1004
QY 281 AspLysThrProLeuThrTrpLeuGlyArgLeuLeuSerAlaGlyPheAlaLeuLeuGly 300
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Db 1005 GACAAACTCCCTTAACCTGGCTGGAGAAATGCTTCTGACAGGCTTTCGACACTCTTGGC 1064
QY 301 IleSerPhePheAlaLeuProAlaGlyIleLeuGlySerGlyPheAlaLeuLysValGln 320
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Db 1065 ATTTCTTTCTTGGACCTTCCTCCGCGCATCTGGCTGAGGTTTGCATTTAAAGATGACAA 1124
QY 321 GluGlnHisArgGlnLysHisPheGluLysArgArgAsnProAlaIleAsnLeuIleGln 340
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Db 1125 GAACACACACCCGACAAACACTTTTGAGAAAGAAAGAAAGAACCCACCTCCCAACTATTCAG 1184
QY 341 CysValIlePheSerThrAlaAlaAspGluLysSerValSerIleAlaThrTrpLysPro 360
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Db 1185 TGTGTTTGGCGTAGTACGACAGCTGATGAGAAATCTGTTCCATTCGCAACCTGGAAGCCA 1244
QY 361 HisLeuLysAlaLeuHisThrCysSerProThrAsnGlnLysLeuSerPheLysGluArg 380
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Db 1245 CACTGGAAGGCTTGACACCTGACAGCCCTACCAATCAAGAGTAAGTTTAAAGGAGCGCA 1304
QY 381 ValArgMetAlaSerProArgGlyGlnSerIleLysSerArgGlnAlaSerValGlyAsp 400
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Db 1305 GTGCCCATGGCGTACGCCGAGGCGCCAGAGTATTAGAGCCGACAAACCTCAGTAGTGAGC 1364
QY 401 ArgArgSerProSerThrAspIleThrAlaGluGlySerProThrLysValGlnLysSer 420
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Db 1365 AGGAGGTCCCGCCAGACGACATCAAGCCGAGGAGGAGTCCCGCCAAAGTCGAGAGAGC 1424
QY 421 TrpSerPheAsnAspArgThrArgPheArgProSerLeuArgLeuLysSerSerGlnPro 440
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Db 1425 TGGACCTTCACAGCAGAACCCGCTTCGCGCTCGCTCGCTCAAAAGTTTTCAGGCCA 1484
QY 441 LysProValIleAspAlaAspThrAlaLeuGlyThrAspAspValIleArgGlyLysGly 460
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Db 1485 AAACGACGATGATGATGCTGACACAGCCCTTGGACATGATGATGATGATGATGATGATG 1544
QY 461 CysGlnCysAspValSerValGluAspLeuThrProProLeuLysThrValIleArgAla 480
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Db 1545 TGGCAGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1604
QY 481 IleArgIleMetLysPheHisValAlaLysArgLysPheLysGluThrLeuArgProTrp 500
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Db 1605 ATCAAGATTTATGAATTTTCAATGTGCAAAACGGAAGTTTAAAGGAACATTTACGTCCAAAT 1664
QY 501 AspValLysAspValIleGlnGlnTrpSerAlaGlyHisLeuAspMetLeuCysArgIle 520
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Db 1665 GATGTAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1724
QY 521 LysSerLeuGlnThrArgValAspGlnIleLeuGlyLysGlyGlnIleThrSerAspLys 540
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Db 1725 AAAAGCCTTCAACACAGGTTGATCAAAATCTTGGAAGAAAGGCAAAATCAATCAGATAGAG 1784
QY 541 LysSerArgGlyLysIleThrAlaGluHisGluThrThrAspAspLeuSerMetLeuGly 560
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Db 1785 AAGAGCCGAGAGAAATTAACAGCAGAACATGAGACACAGACGATCTCAGATGCTCGGT 1844
QY 561 ArgValValLysValGluLysGlnValGlnSerIleGlySerLysLeuAspCysLeuLeu 580
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Db 1845 CGGTTGGTCAAGGTTGAAAACAGGTACAGTCCATAGATCCAGCTGACTGCTTACTA 1904
QY 581 AspIleTrpGlnGlnValIleuArgLysGlySerAlaSerAlaLeuAlaLeuAlaSerPhe 600
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Db 1905 GACATCTATCAACAGGCTTCGGAAGGCTCTGCTCAGCCCTGCTTGGCTTCATTC 1964
QY 601 GlnIleProProPheGluCysGluGlnThrSerAspTrpGlnSerProValAspSerLys 620
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Db 1965 CAGATCCACCTTTTGAATGTGAACAGACATCTGACATCAAAAGCCGTGGATGACAAA 2024
QY 621 AspLeuSerGlySerAlaGlnAsnSerGlyCysLeuSerArgSerThrSerAlaAsnIle 640
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Db 2025 GATCTTTGCGGTTCCGCAACAAACAGTGGCTGATTATCAGATCAACATAGTCCAAACATC 2084
QY 641 SerArgGlyLeuGlnPheIleLeuThrProAsnGluPheSerAlaGlnThrPheTrpAla 660
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Db 2085 TCGAGAGGCTCGAGTTCATCTCTGCGCAAAATGATGATGATGATGATGATGATGATGATG 2144
QY 661 LeuSerProThrMetHisSerGlnAlaThrGlnValProIleSerGlnSerAspGlySer 680
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Db 2145 CTTAGCCCTACTATGACACAGTACACACACACACACACACACACACACACACACACACAC 2204
QY 681 AlaValAlaAlaIleThrAsnThrIleAlaAsnGlnIleAsnThrAlaProLysProAlaAla 700
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Db 2205 GCAGTGGAGGACACACACACACACATTCGCAAAATTAATTAATTAATTAATTAATTAATTA 2264
QY 701 ProThrThrLeuGlnIleProProProLeuProAlaIleLysHisLeuProArgProGlu 720
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Db 2265 CCAACAACTTTACAGATCCACCTCTCTCCAGCCATCAAGACATCTGCCAGGCCAGAA 2324
QY 721 ThrLeuHisProAsnProAlaGlyLeuGlnGlnSerIleSerAspValIleThrCysLeu 740
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Db 2325 ACTCTGACCCCTTAACCTCGACGAGCTTACAGGAAGACATTTCTGACGCTCACCCCTGCTT 2384
QY 741 ValAlaSerLysGluAsnValGlnValAlaGlnIleAsnAsnLeuThrLysAspArgSerMet 760
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Db 2385 GTTGCTTCGCAAGAAATGTTTCAGAGTTCACAGTCAAAATCTCACCAAGAGACGTTCTAG 2444
QY 761 ArgLysSerPheAspMetGlyGlyGluThrLeuLeuSerValCysProMetValProLys 780
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Db 2445 AGGAAAGCCTTTGACATGGGAGGAGAAACCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2504
QY 781 AspLeuGlyLysSerLeuSerValGlnAsnLeuIleArgSerThrGluGluLeuAsnIle 800
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Db 2505 GACTTGGGCAATCTTTGTCTGTGCAAAACCTGATCAGATGACCGAGAGACATGATATATA 2564
QY 801 GlnLeuSerGlySerGluSerSerGlySerArgGlySerGlnAspPheTrpProLysTrp 820
|||||
Db 2565 CAACCTTCAGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2624
QY 821 ArgGluSerLysLeuPheIleThrAspGluGluValGlyProGluGluThrGluThrAsp 840
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QY	261	SetrThTyAlaAspAlaLeuTPrtPrgLyThrIleThrLeuThrThrIleGlyTyrcly	280
Db	781	TCThACATATGCAATAGCTCTCTGTGGGCAATTCATTCATGACAACTATTGGCTATGCA	840
QY	281	AspLysThrProLeuThrTrpPleuGLArgLeuLeuSerAlaGlyPheAlaLeuLeuGly	300
Db	841	GACAAACCTCCCTACTGTCGTGGGAGATGCTTTTCTGAGGCTTTGCACCTCTGGC	900
QY	301	IleSerPhePheAlaLeuProAlaGlyIleLeuGlySerGlyPheAlaLeuLysValGln	320
Db	901	ATTCTTCTTCTTGCACCTCTCCCGCGCATCTTGGCTACGTTTGGCATTTAAAGTACAA	960
QY	321	GluGlnHisArgGlnLysHisPheGlnLysArgArgAsnProAlaAlaAsnLeuIleGln	340
Db	961	GAACAACACCGCCAGAAACCTTTGAAGAAAAAGAAAGAACCCAGCTGCCAACCTCTTAG	1020
QY	341	CysValTrpArgSerTrpAlaAlaAspGluLysSerValSerIleAlaThrTrpLysPro	360
Db	1021	TGTGTTGGGTAGTTAAGCAGCTGATGAGAAATCTGTTTCATTGCACTCGAAGCCA	1080
QY	361	HisLeuLysAlaLeuHisThrCysSerProThr-----	371
Db	1081	CACCTTAAGGCTTGGACACCTGCGACCTTACCAAGAAAGAACAGGAGCATCAACG	1140
QY	372	AsnGlnLysLeuSerPheLysGluArgValArgMetIleSerProArgGlyGlnSerIle	391
Db	1141	AGTCACAAAGCTAAGTTTAAAGAGCGAGTGGCGAGCTACCCGAGGGGCAAGATTT	1200
QY	392	LysSerArgGlnAlaSerValGlyAspArgArgSerProSerThrAspIleThrAlaGln	411
Db	1201	AAGAGCGCAACACCTCAGTAGGAGACAGAGATGCCCAACGACCGCATCACAGCCAG	1260
QY	412	GlySerProThrLysValGlnLysSerTrpSerPheAsnAspArgThrArgPheArgPro	431
Db	1261	GGCAGAGCCCAACCAAGTGCAGAAAGAGCTGGAGCTTCAACGCAACCCGCTCGGCCC	1320
QY	432	SerLeuArgLeuLysSerSerGlnProLysProValIleAspAlaAspThrAlaLeuGly	451
Db	1321	TGGCTGCGCTCAAAAGTTCTGACGCCAAACCAAGTGAAGTGGTGACACGCGCTTGGC	1380
QY	452	ThrAspAspValTrpArgSpGluLysGlyCysGlnCysAspValSerValGluAspLeuThr	471
Db	1381	ACTGATGATGTATATGATGAAAAAGATGCCAGTGATATGATAGTGGAGAACTCTACC	1440
QY	472	ProProLeuLysThrValIleArgAlaIleArgIleMetLysPheHisValAlaLysArg	491
Db	1441	CCACCACTTAAACTCTCATCTCAGCATATCGAATTTGAATTTCAATGTGCAAAACGG	1500
QY	492	LysPheLysGluThrLeuArgProTrpArgAspValLysAspValIleGluGlnTrpSerAla	511
Db	1501	AGGTTTAAGAAACGTTACCTCCATATGATGTTAAAGATGTCATTGAAACAATATTTGCT	1560
QY	512	GlyHisLeuAspMetLeuCysArgIleLysSerLeuGlnThrArgValAspGlnIleLeu	531
Db	1561	GGTCAATCTGCAATGTTGTGTAAATTAAGCCTTCAACACGCTGTGATCAAAATCTT	1620
QY	532	GlyLysGlyGlnIleThrSerAspLysLysSerArgGluLysIleThrAlaGluHisGln	551
Db	1621	GGAAAAAGGCAATCAATCAGATTAAGAAAGCCGAGAGAAAAATMACAGCGAACAATGAG	1680
QY	552	ThrThrAspAspLeuSerMetLeuGlyArgValValLysValGluLysGlnValGlnSer	571
Db	1681	ACCACAGACGATCTCGATATGCTCGGTGGGTGTCAAGTTGAAAAACAGTACAGTCC	1740
QY	572	IleGluSerLysLeuAspCysLeuLeuAspIleTyrlGlnGlnValLeuArgLysGlySer	591
Db	1741	ATAGAGTCCAAAGCTGAGTGCCTACTAGACATCTATCAACAGGTCCTTGGAAAGGCTCT	1800
QY	592	AlaSerAlaLeuAlaLeuAlaSerPheGlnIleProProPheGluCysGluGlnThrSer	611
Db	1801	GGCTAGGCGCTTGCTTGGCTTCATTCACGATCCCAACCTTTGAATGTGAACAGACATCT	1860

QY	612	AspTyrGlnSerProValaspSerLysAspLeuSerGlySerIleAlaGlnAsnSerGlyCys	631
Db	1861	GACTATCAAGAAGCCCTGTGGATACCAAGAATCTTTCGGGTTCGCCACAAACACAGTGGCTGC	1920
QY	632	IleSerArgSerThrSerIleAsnIleSerArgGlyLeuGlnIleIleLeuThrProAsn	651
Db	1921	TTATCCAGATCAACTAGTGTCCAAATCTCGAGAGGCTCGAGTTTCATTTCGAGGCCAAAT	1980
QY	652	GluPheSerAlaGlnThrPheTyrAlaLeuSerProThrMetHisSerGlnIleArgGln	671
Db	1981	GAGTTCAGTGGCCAGACTTCTACCGCGCTTAGGCCCTACTGTACAGTCAAGCAACACAG	2040
QY	672	ValProIleSerGlnSerAspGlySerAlaValAlaAlaThrAsnThrIleAlaAsnGln	691
Db	2041	GGGCCAATTAGTCAAAAGCGATGGCTGAGAGTGGAGCCACCAACACCATTTGCCAAACCA	2100
QY	692	IleAsnThrAlaProLysProAlaAlaProThrThrLeuGlnIleLeuProProLeuPro	711
Db	2101	ATTAAATACGGCACCCCAAGCAGCAGGCCCCACACAACTTACAGATTCACACTCTCTCCCA	2160
QY	712	AlaIleLeuHisLeuProArgProGluThrLeuHisProAsnProAlaGlyLeuGlnGlu	731
Db	2161	GCCATCAACCACTGTGCCAGGCCAGCAAACTGTGCACCTCAACCTCGACGCTTACAGAA	2220
QY	732	SerIleSerAspValThrThrCysLeuValAlaSerLysGlnAsnValGlnValAlaGln	751
Db	2221	ACCATTTCTGAGCGTCCACCACTGCTGTGGCTTCACAGAAATGTTCAGTTGGACAG	2280
QY	752	SerAsnLeuThrLysAspArgSerMetArgLysSerPheAspMetGlyGlyGluThrLeu	771
Db	2281	TCAAAATCCACCAAGACCGCTTCTATGAGGAAAGCTTTGACATGGGAGAGAAACTCTG	2340
QY	772	LeuSerValCysProMetValProLysAspLeuGlyLysSerLeuSerValGlnAsnLeu	791
Db	2341	TGTCTGTGTCTGCCAATGTGTGCCGAAGCACTGGGCCAAATCTTGTCTGTGCAAAACCTG	2400
QY	792	IleArgSerThrGluGluLeuAsnIleGlnLeuSerGlySerGluSerGlySerArg	811
Db	2401	ATCAGGTCACCCAGCAGCACTGATATACAACTTTCAGGGAGTGCATCAAGTGGCTCCAGA	2460
QY	812	GlySerGlnAspPheTyrProLysTrpArgGlySerLysLeuPheIleThrAspGluGlu	831
Db	2461	GGCACGCCAAGATTTTATCCCCAAATGGAGGGAATCCAAATTTGTTTATCACTGATGAAGAG	2520
QY	832	ValGlyProGluGluThrGluThrAspThrPheAspAlaAlaProGlnProAlaArgGlu	851
Db	2521	GTGGGTCCCGAAGACAGACAGACACTTTTGATGCCGCAACCGCAGCTGCCAGGAA	2580
QY	852	AlaAlaPheAlaSerAspSerLeuArgThrGlyArgSerArgSerSerGlnSerIleCys	871
Db	2581	GCTGCTTGTGATCGACACTCTTAAGAGCTGGAAGGCTCAGATCACTCAAGACATTGTGT	2640
QY	872	LysAlaGlyGlySerThrAspAlaLeuSerLeuProHisValLysLeuLys	888
Db	2641	AAGGACGAGGAAGATACAGATCCTCCCTGACCTTGCCCATGCTCAAACTGAAA	2691
RESULT 5			
AAD27192			
ID	AAD27192	standard; cDNA; 2694 BP.	
AC	AAD27192;		
XX			
DT	09-APR-2002	(first entry)	
DE		Human potassium channel polypeptide, KCNQ5 cDNA.	
KW		Human; potassium channel polypeptide; KCNQ5; pain; migraine; stroke;	
KW		dementia; triuma; epilepsy; seizure; amyotrophic lateral sclerosis;	
KW		ALS; multiple sclerosis; MS; Parkinson's disease; ataxia; depression;	
KW		anxiety disorder; bipolar disorder; sleep disorder; eating disorder;	
KW		addiction; myokymia; Alzheimer's disease; age-associated memory loss;	
KW		learning deficiency; cognitive disorder; motor disease; neuron disease;	
KW		neuropysiological disorder; neuropsychological disorder; asthma;	

Db 1201 AAGAGCCGACAAAGCCTCAGTAGGTGACAGAGAGTCCCAAGCAGCATCATCACCAG 1260
 QY 412 GlySerProThrIleValGlnLysSerIlePheAsnAspArgThrArgPheArgPro 431
 Db 1261 GGCGATGCCACCAAGATGTCACAGAGGCTGGAGCTTCAACGACGACCCGCTCGGCGCC 1320
 QY 432 SerIleuArgIleuLysSerSerGlnProLysProValIleAspAlaSerThrAlaLeuGly 451
 Db 1321 TCGCTGGCCCTCAAAAGATCTCAGCCCAAAACCATGATAGATGCTGACACAGCCCTTGGC 1380
 QY 452 ThrAspAspValTyrAspGluLysGlyCysGlnCysAspValSerValGluAspLeuThr 471
 Db 1381 ACTGATGATGATATGATGATAAAAGATGCCAGTGTGATGATCATGAGGAAGACCTCACC 1440
 QY 472 ProProLeuLysThrValIleArgAlaIleArgIleMetLysPheHisValAlaLysArg 491
 Db 1441 CCACCACTTAAACCTGATTCAGCTATCAGATATGAAATTTCAATGTGCAAAACGG 1500
 QY 492 LysPheLysGluThrIleuArgProTyrAspValLysAspValIleGluGlnTyrSerAla 511
 Db 1501 AAGTTAAAGAAAGCTTACGCTCATATGATGTAAAGATGTCAATGCAATATTCCT 1560
 QY 512 GlyHisIleuAspMetLeuLysArgIleLysSerLeuGlnThrArgValAspGlnIleu 531
 Db 1561 GGTCACTGACATGTTGTGTAATTAAGCCTTCAACACGCTGTGATCAAAATTCCT 1620
 QY 532 GlyLysGlyGlnIlePheSerAspLysLysSerArgGluLysIleThrAlaGluHisGln 551
 Db 1621 GGAAAAAGGCAAAATCACATCAGATTAAGAAAGCCGAGAAATAACACAGACATGAG 1680
 QY 552 ThrThrAspAspLeuSerMetLeuGlyArgValValLysValGluLysGlnValGlnSer 571
 Db 1681 ACCACAGACGATCTCAGATGCTCGGTGGGTGTCAGAGTTGAAAAACAGGTACAGTCC 1740
 QY 572 IleGluSerLysIleuAspCysLeuLysAspIleTyrGlnGlnValLeuArgLysLysSer 591
 Db 1741 ATAGAGTCCAAAGCTGAGCTGCTACTAGATCAATCAAAACAGGCTCTCGGAAAGGCTCT 1800
 QY 592 AlaSerAlaLeuAlaLeuAlaSerPheGlnIleProPheGluCysGlnIleThrSer 611
 Db 1801 GCCACAGCCCTCGCTGGCTTCAATCCAGATCCACCTTTTGAAATGGAACAGACATCT 1860
 QY 612 AspThrGlnSerProValAspSerLysAspLeuSerGlySerAlaGlnAsnSerGlyCys 631
 Db 1861 GACATATAAAGCCCTGTGGATGAGCAAGATCTTTCGGGTTCCGACAAACAGAGGCTCGC 1920
 QY 632 LeuSerArgSerThrSerAlaAsnIleSerArgGlyLeuGlnPheIleLeuThrProAsn 651
 Db 1921 TTATCCAGATCACTAGTGCACATCTCAGAGGCTGCAATTCATCTGACGCCAAT 1980
 QY 652 GluPheSerIleGlnThrPheTyrAlaLeuSerProThrMetHisSerGlnAlaThrGln 671
 Db 1981 GAGTTAGTGGCCAGACTTCTACGGCTTACGCCCTACTATGACAGATCAAGCAACAG 2040
 QY 672 ValProIleSerGlnSerAspGlySerAlaValAlaIleAsnThrIleAlaAsnGln 691
 Db 2041 GTGCCAATTAGTCAAAAGCATGGCTCAGCAGTGGCAGCCCAACACCATTTGCAAAACCA 2100
 QY 692 IleAsnThrAlaProLysProAlaAlaProThrThrLeuGlnIleProProLysPro 711
 Db 2101 ATAAATACGGCCAGCAAGCAGACGCCCAACAACTTTACAGATCCACCTCTCTCCCA 2160
 QY 712 AlaIleLysHisLeuProArgProGluThrIleuHisProAsnProAlaGlyLeuGlnGln 731
 Db 2161 GCCATCAAGCATCTGCCAGGCCAGAAACTTGCACCCCTAACCCCTCAGCTTACAGGAA 2220
 QY 732 SerIleSerAspValThrThrCysLeuValAlaSerLysGlnAsnValGlnValAlaGln 751
 Db 2221 AGCATTTTGTGACGTCACACACCTGCTTGTGCTCCAGAGAAATGTTTCAGGTTCACAG 2280
 QY 752 SerAsnLeuThrLysAspArgSerMetArgLysSerPheAspMetGlyGluThrIleu 771
 Db 2281 TCAATCTCACCAAGAGCGTTCTATGAGAAAGCTTTCAGATGGAGGAACCTCTG 2340

QY 772 LeuSerValCysProMetValProLysAspLeuGlyLysSerLeuSerValGlnAsnLeu 791
 Db 2341 TTGCTGCTCTCCCATGCTGGCCGAAGACATGGGCAATCTTGTCTGTGCAAAACCTG 2400
 QY 792 IleArgSerThrGluGluLeuAsnIleGlnIleuSerGlySerGluSerSerGlySerArg 811
 Db 2401 ATCAGGTGACCGAGGAACCTAATATACACTCTTCAGGAGTGAAGTCAAGTGGCTCCAGA 2460
 QY 812 GlySerGlnAspPheTyrProLysTyrArgGluSerLysLeuPheIleThrAspGlnGln 831
 Db 2461 GGCGCCCAAGATTTTACCCCAATGAGGGAATCCAAATGTTTATACATGATGAAGAG 2520
 QY 832 ValGlyProGluGluThrGluThrAspThrPheAspAlaAlaProGlnProAlaArgGln 851
 Db 2521 GTGGTCCCGAAGACAGACAGACACTTTTGATCCCGCAGCGACCTGCCAGGGAA 2580
 QY 852 AlaAlaPheAlaSerAspSerLeuArgThrGlyArgSerArgSerSerGlnSerIleCys 871
 Db 2581 GCTGCCCTTTCATCAGACTCTTAAGCATGGAAGTCAAGATCATCTCAGACCATTTGT 2640
 QY 872 LysAlaGlyLysSerThrAspAlaLeuSerLeuProHisValLysLeuLys 888
 Db 2641 AAGCAGAGAAAGTACAGATGCCCTCAGCTTCTCATGTCAAACTGAA 2691

RESULT 6

ID AAC85414 standard; cDNA: 3137 BP.

XX AAC85414;

DT 20-APR-2001 (first entry)

DE Human KCNQ5 potassium channel subunit coding sequence.

KW Human; KCNQ5; heteromeric channel; chromosome 6; Parkinson's disease;
 KW central nervous system; CNS; Alzheimer's disease; anxiety; ataxia;
 KW CNS damage; trauma; stroke; neurodegenerative illness; schizophrenia;
 KW compulsive behaviour; dementia; depression; Huntington's disease;
 KW mania; memory impairment; memory dysfunction; Huntington's disease;
 KW phobia; pick's disease; psychosis; stroke; tremor; seizure; convulsion;
 KW epilepsy; ds.
 KW OS Homo sapiens.
 XX

FX Key Location/Qualifiers

FT 1..2694

FT CDS /*tag= a

FT /product= "KCNQ5 subunit"

PN WO200077035-A2.

PD 21-DEC-2000.

PF 29-MAY-2000; 2000MO-DK00289.

PR 11-JUN-1999; 99DK-0000828.

PA (NEUR-) NEUROSEARCH AS.

PI Jentsch TJ.

DR WPL: 2001-080678/09.

DR P-PSDB: AAB47046.

XX

PT Novel genes encoding KCNQ5 potassium channel subunits, useful for

PT treating Alzheimer's disease, anxiety, ataxia, stroke, dementia,

PT depression, Huntington's disease, schizophrenia and Parkinson's disease

PS Claim 2; Page 44-48; 50pp; English.

XX This sequence encodes the human KCNQ5 protein. The KCNQ5 protein forms

CC heteromeric channels with other KCNQ channel subunits, in particular
CC KCNQ3 and KCNQ4. The KCNQ5 gene has been localised to the long arm of
CC chromosome 6 (q44). Chemicals which have the ability to bind to
CC KCNQ5 are useful for diagnosis, treatment, prevention or alleviation
CC of diseases related to diseases or adverse conditions of the central
CC nervous system (CNS), including affective disorders, Alzheimer's
CC disease, anxiety, ataxia, CNS damage caused by trauma, stroke or
CC neurodegenerative illness, cognitive deficits, compulsive behavior,
CC dementia, depression, Huntington's disease, mania, memory impairment,
CC memory disorders, memory dysfunction, motion disorders, motor
CC disorders, neurodegenerative diseases, Parkinson's disease and
CC Parkinson-like motor disorders, phobias, pick's disease, psychosis,
CC schizophrenia, spinal cord damage, stroke, tremor, seizures,
CC convulsions and epilepsy.

XX Sequence 3137 BP; 865 A; 749 C; 745 G; 778 T; 0 other;

Alignment Scores:

Pred. No.:	0	Length:	3137
Score:	4527.50	Matches:	887
Percent Similarity:	99.00%	Conservative:	1
Best Local Similarity:	98.89%	Mismatches:	0
Query Match:	99.57%	Indels:	9
DB:	22	Gaps:	1

US-09-810-796-5 (1-888) x AAC85414 (1-3137)

QY 1 MellysaspValGluSerGlyArgGlyArgValLeuLeuAsnSerAlaAlaAlaArgGly 20
Db 1 ATGAGAGATGTGGAGTGGGGCCGGGGGAGGGTGTCTGTAAGTCCGGACCCGCGGGGCG
QY 21 AspGlyLeuLeuLeuLeuGlyThrArgAlaAlaThrLeuGlyGlyGlyGlyGlyLeu 40
Db 61 GACGGCTGCTACTGCTGCTGGCACCAGCCGCGGCGCAGCTGGTGGCGGGGGTGGCTTG
QY 41 ArgGlySerArgArgGlyLysGlnGlyAlaArgMetSerLeuLeuGlyLysProLeuSer 60
Db 121 AGGAGAGAGCCCGCGGCGAAGCAGGAGGCGCGGATGAGCTGTGGGAGAGCCGCTCT
QY 61 TyrThrSerSerGlnSerCysArgArgAsnValLysTyrArgArgValGlnAsnTyrLeu 80
Db 181 TACACGAGTACCGAGAGTCCGGCGCAACGTCAAGTACCGCGGGGTGCACAACTACTG
QY 81 TyrAsnValLeuGluArgProArgGlyTyrPalaPheIleTyrHisAlaPheValPheLeu 100
Db 241 TACACGAGTGGAGAGAGCCCGCGGCGTTCATCTACACAGCTTTCGTTTTCTC
QY 101 LeuValPheGlyCysLeuIleLeuSerValPheSerThrIleProGluHisThrLysLeu 120
Db 301 CTGTCTTGTGCTGATTTGTTCAGTGTTCATCCATCCCGAGACACACAATAATTG
QY 121 AlaSerCysLeuLeuIleLeuGluPheValMetIleValValPheGlyLeuGluPhe 140
Db 361 GCGTCAAGTCCCTCTGATCTGGAGTTCGTGATGATTCGTCTTGTGGAGTTC
QY 141 IleIleArgIleTyrPserAlaGlyCysCysArgTyrArgGlyTyrPrlGlnGlyArgLeu 160
Db 421 ATCAATGCAATCTGGTGGCGGTTGCTGTGTGATGATGAGAGATGGCAAGAGACTG
QY 161 ArgPheAlaArgLysProPheCysValIleAspThrIleValLeuIleAlaSerIleAla 180
Db 481 AGGTTGCTCAAGACCTCTGCTGTATAGATACCAATGTTCTTAATGCTCAATAGCA 540
QY 181 ValValSerAlaValThrGlnGlyAsnIlePheAlaThrSerAlaLeuArgSerLeuArg 200
Db 541 GTTGTTTTCGAAAAACTCAGGGTAAATTTTTCGACAGTCTGCAAGAGTCTCCCT
QY 201 PheLeuGlnIleLeuArgMetValArgMetAspArgArgGlyGlyThrTyrLysLeuLeu 220
Db 601 TTCCTACAGATCCTCCGATGGTGGCAGATGACCAAGGAGGAGCACTTGCAAATTACTG 660
QY 221 GlySerValValTyrAlaHisSerLysGluLeuIleThrAlaTyrTyrIleGlyPheLeu 240

Db 661 GCTTCAGTGGTTATGTCTCACAGCAAGGAATTAATCACAGCTTGATCATAGCATTTTG 720
QY 241 ValLeuIlePheSerSerPheLeuValTyrLeuValGluLysAspAlaAsnLysGluPhe 260
Db 721 GTTCTTAATTTTTTGTCTTTCCTTGTCTATGTGGGAGAAAGAGCAATPAAGAGTTT
QY 261 SerThrTyrAlaAspAlaLeuThrPrlGlyThrIleThrLeuThrIleGlyTyrGly 280
Db 781 TCTACATGTGCAGATGCTCTGTGGGGGACAAATTCATTTGACAACTATTTGGCATGGA 840
QY 281 AspLysThrProLeuThrTyrPrlGlyArgLeuLeuSerAlaGlyPheAlaLeuLeuGly 300
Db 841 GACAAACTCCCTTAACCTTGGCTGGAGATGCTTCTGCAGCGCTTGCACTCCTTGGC 900
QY 301 IleSerPhePheAlaLeuProAlaGlyIleLeuGlySerGlyPheAlaLeuLysValGln 320
Db 901 ATTTCTTTCTTGGACCTTCGCGGCAATTCCTGGCTGAGGTTTGGCAATTAAGATACAA 960
QY 321 GluGlnHisArgGlnLysHisPheGluLysArgArgAsnProAlaAlaAsnLeuIleGln 340
Db 961 GACACACACCCCGCAAAACACTTTGAGAAAGAAAGAACCCAGCTGCCAATCTCATTCAG 1020
QY 341 CysValTyrPargSerTyrAlaAlaAspGluLysSerValSerIleAlaThrTyrLysPro 360
Db 1021 TGTGTTGGCGTAGTTACGACGCTGATGAGAAATCTGTTCATTTGCAACCTGGAAGCA 1080
QY 361 HistLeuLysAlaLeuHisThrCysSerProThr----- 371
Db 1081 CACTGAGAGGCTTGTACACACTGCGAGCCCTACCAAGAAAGAAAGGAGAGCATCAAC 1140
QY 372 AsnGlnLysLeuSerPheLysGluArgValArgMetAlaSerProArgGlyGlnSerIle 391
Db 1141 AGTCAAGAGCTAAGTTTAAAGAGGAGAGTCCCATGGCTAGCCCAAGGGGCGAGTAT 1200
QY 392 LysSerArgGlnAlaSerValGlnLysPargArgSerProSerThrAspIleThrAlaGlu 411
Db 1201 AAGACCCGCAAGCCTCAGTAGTACAGGAGGCTCCCAAGCAGCAGATCCACCCGAG 1260
QY 412 GlySerProThrLysValGlnLysSerThrPserPheAsnArgThrArgPheArgPro 431
Db 1261 GGCAGTCCCAAAAGTGCAGAAAGAGCTGGAGCTTCMACGACCGAACCCTCCGGGCC 1320
QY 432 SerLeuArgLeuLysSerSerGlnProLysProValIleAspAlaAspThrAlaLeuGly 451
Db 1321 TCGCTCGCGCTCAAAAGTTCACAGCCAAACCAAGATGATGATGACACACCTTGCC 1380
QY 452 ThrAspAspValTyrAspGluLysGlyGlnCysAspValSerValGluLysLeuThr 471
Db 1381 ACTGATGATGATATGATGAAAAAGAGATGCCAGTGTGATGATGAGAGAGACCTCACC 1440
QY 472 ProProLeuLysThrValIleArgAlaIleArgIleMetLysPheHisValAlaLysArg 491
Db 1441 CCACCACTTAAACGTCTCATTTGACCTATCACAATTAATTAATTTTCATGTCCAAAACGG 1500
QY 492 LysPheLysGluThrLeuArgProTyrAspValLysAspValIleGluGlnTyrSerAla 511
Db 1501 AAGTTTAAGAAACATTAACGTCCATATGATGTAAGAAAGATGATGATGAACAAATTCCTGCT 1560
QY 512 GlyHisLeuAspMetLeuCysArgIleLysSerLeuGlnThrArgValAspGlnIleLeu 531
Db 1561 GGTCACTGTGCAGATGTGTGTAGAAATTAAGCCTTCAACACGAGTTGATCAAAATTTCT 1620
QY 532 GlyLysGlyGlnIleThrSerAspLysLysSerArgGluLysIleThrAlaGlnHisGlu 551
Db 1621 GGAAGAGGCAATCACAATCAGATGAAGAGACCCGAGAGAAATTAACACAGCAACTGAG 1680
QY 552 ThrThrAspAspLeuSerMetLeuGlyArgValValLysValGluLysGlnValGlnSer 571
Db 1681 ACCACAGAGATCTCAGTATGCTCGGTCCGGTGCACAAAGTTGAAAAACAGATACAGTCC 1740
QY 572 IleGluSerLysLeuAspCysLeuLeuAspIleTyrGlnGlnValLeuArgLysGlySer 591
Db 1741 ATGAAATCCAAAGTGGAGTGCCTACTAGACATCTATCAACACAGCTCTTGGAAAGGCTCT 1800

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QY 592 AAlaSerAlaLeuAlaLeuAlaSerPheGlnIleProProPheGluGluGlnThrSer 611
    |||
Db 1801 GCCTAGGCCCTCGCTTTGGCTTCATTCAGATCCACCTTTTGAATGTAAGACGACATCT 1860
QY 612 AspTyrGlnSerProValaAspSerLysAspLeuSerGlySerAlaGlnAnsSerGlyCys 631
    |||
Db 1861 GACTATCAAGCCCTGTGGATAGCAAGATCTTCCGGTTCGACCAAAACAGTGGCTGC 1920
QY 632 LeuSerArgSerThrSerAlaAnsIleSerArgGlyLeuGlnPheIleLeuThrProAsn 651
    |||
Db 1921 TTATTCAGATCACTAGTAGCCACATCTCGAGAGGCTCAGTCTATCTGACGCCAAAT 1980
QY 652 GluPheSerAlaGlnThrPheTyrAlaLeuSerProThrMetHisSerGlnAlaThrGln 671
    |||
Db 1981 GAGTTCAGTGGCCCAACATCTTACGGCGTTACCCCTACATGACAGTCAAGACACACAG 2040
QY 672 ValProIleSerGlnSerAspGlySerAlaValAlaAlaThrAsnThrIleAlaAsnGln 691
    |||
Db 2041 GTGCCAATTAGTCAAAAGGATGGCTCAGCAGTGCAGCCACCAACACCATTCGAAACCA 2100
QY 692 IleAsnThrAlaProLysProAlaAlaProThrThrLeuGlnIleProProIlePro 711
    |||
Db 2101 ATTAATACGGACCAACCAACCCAGACCCCAACACTTTACAGATCCACCTCCTCCCA 2160
QY 712 AlaIleLysHisLeuProArgProGluThrLeuHisProAsnProAlaGlyLeuGlnGlu 731
    |||
Db 2161 GCCATCAAGCATCTGCCAGGCGACAAACTCGACACCTTCAGAGCTTACAGGAA 2220
QY 732 SerIleSerAspValThrThrCysLeuValAlaSerLysGlnAsnValGlnValaGln 751
    |||
Db 2221 AGCATTTCTGACGCACACCATCGCTTGTGCTCCCAAGGAAATGTTCCAGGTTGCACAG 2280
QY 752 SerAsnLeuThrLysAspArgSerMetArgLysSerPheAspMetGlyGlyGluThrLeu 771
    |||
Db 2281 TCAATCTCACCAGGACCGCTTCTATGAGGAAACCTTTGACATGGAGAGAAACTCTG 2340
QY 772 LeuSerValCysProMetValProLysAspLeuGlyLysSerLeuSerValGlnAsnLeu 791
    |||
Db 2341 TTGCTCTCTGTCCCATGCTGCTCCGAAAGACTTGGCAAACTTTGCTGTGCAAAACCTG 2400
QY 792 IleArgSerThrGluGluLeuAsnIleGlnLeuSerGlySerGlnSerSerArg 811
    |||
Db 2401 ATCAGGTCGACCGAGGAACTAAATATACAACTTTCAGGAGTCAAGTGGCTCCCAA 2460
QY 812 GlySerGlnAspPheTyrProLysTrpArgLysLeuSerLysPheIleThrAspGluGlu 831
    |||
Db 2461 GGCAGCCCAAGATTTTACCCCAATGAGGAGATCCCAATTTCTTATTAATCATGAAGAG 2520
QY 832 ValGlyProGluGluThrGluThrAspThrPheAspAlaAlaProGlnProAlaArgGlu 851
    |||
Db 2521 GTGGGTCCCGAAGAGACAGACACTTTTGATGCCGACCCAGCCTCCAGGAGAA 2580
QY 852 AlaAlaPheAlaSerAspSerLeuArgThrGlyArgSerArgSerSerGlnSerIleCys 871
    |||
Db 2581 GCTGCTCTTTCATGATGACTCTTAAGGACTGTGAAGCTACCATCTTCAGAGCAATTTGT 2640
QY 872 LysAlaGlyLeuSerThrAspAlaLeuSerLeuProHisValLysLeuLys 888
    |||
Db 2641 AAGGAGAGAAAGTACAGATGCCCTCAGCTTGCTCATGTCAAACTGAAA 2691

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RESULT 7
AAS14651
ID AAS14651 standard; cDNA; 3071 BP.
XX
AC AAS14651;
XX
DT 18-DEC-2001 (first entry)
XX
DE Human cDNA for voltage gated potassium channel hKvN05.
XX
KW Human; ss; voltage-gated potassium channel; hKCN05; nootropic;
cerebroprotective; neurotropic; analgesic; vision disorder;

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KW central nervous system disorder; epilepsy; migraine; hearing disorder;
KW psychotic disorder; seizure; learning disorder; memory disorder;
KW stroke; pain; gene therapy.
OS Homo sapiens.
PN WC200170759-A1.
XX
PD 27-SEP-2001.
XX
PF 20-MAR-2001; 2001WO-US09328.
XX
PR 21-MAR-2000; 2000US-190954P.
XX
PA (ICAGEN) ICAGEN INC.
XX
PI Jegla TJ;
XX
DR WPI; 2001-611467/70.
XX
PS Claim 5; Page 61-62; 78pp; English.
XX
CC The invention relates to an isolated polypeptide comprising an
CC alpha-subunit of a KCNQ potassium channel, with a subsequence having
CC 65% sequence identity to amino acids 343-640 of hKCN05-1 amino acid
CC sequence and forms a KCNQ potassium channel having the characteristic of
CC voltage-gating with at least an additional KCNQ alpha-subunit. Also
CC included in the scope of the invention are the nucleic acids encoding
CC hKCN05 (including splice variants encoding hKCN05-1 and hKCN05-2),
CC expression vectors encoding them, antibodies against them, the use of
CC 3-dimensional computer modelling to identify molecules that bind to a
CC KCNQ containing potassium channel and modulate ion flux through the
CC channel. The KCNQ polypeptide is useful for identifying a compound that
CC increases or decreases ion flux through a potassium channel expressed in
CC a eukaryotic host cell or cell membrane. The compound (and the
CC KCNQ nucleic acid when used in gene therapy) is useful as
CC a pharmaceutical agent for treating diseases involving abnormal ion flux,
CC such as disorders of the central nervous system, such as epilepsy,
CC migraines, hearing and vision problems, psychotic disorders, seizures,
CC learning and memory disorders, stroke and pain. The antibodies are
CC useful for detecting a KCNQ5 polypeptide in a human tissue and the
CC use of a nucleotide sequence of KCNQ5 to search computer databases to
CC find variants of the sequence which are associated with disease states,
CC is useful for screening mutations of KCNQ5. The present sequence is
CC a representative cDNA for hKCN05.
XX
SQ Sequence 3071 BP; 849 A; 734 C; 737 G; 750 T; 1 other:

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Alignment Scores:

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Pred. No.: 0 Length: 3071
Score: 4523.50 Matches: 886
Percent Similarity: 98.89% Conservative: 1
Best Local Similarity: 98.77% Mismatches: 1
Query Match: 99.488 Indels: 9
DB: 22 Gaps: 1

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US-09-810-796-5 (1-888) x AAS14651 (1-3071)

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QY 1 MetLysAspValGluSerGlyArgGlyArgValLeuLeuAsnSerAlaAlaAlaArgGly 20
    |||
Db 10 ATCAAGAGATGTGAGTGGGCGCGGCGAGGCTGCTGCTGAACTCGCAAGCCGAGGGGC 69
QY 21 AspGlyLeuLeuLeuLeuGluGlyThrArgAlaAlaThrLeuGlyGlyGlyGlyGlyLeu 40
    |||
Db 70 GACGGCTGCTACTGCTGGGACCCGCGGCGGCAAGCTTGCTGGCGGCGGCGGCTG 129
QY 41 ArgGluSerArgArgGlyLysGlnGlyAlaArgMetSerLeuLeuGlyLysProLeuSer 60
    |||

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Db	130	AAGGAGAGCCCCGGGGGCAAGCAGGGGGGCCGGATGACGCTGCTGGGGGAAGCCCTCTCT	189
Oy	61	TyrThrSerSerClnSerCysAraArgAsnValLysTyrArgValGlnAsnTyrLeu	80
Db	190	TACAGCAGTAGGACAGAGCTGCCGGCCCAAGTCAGTACCGCGGGGTGACAACTACTCG	249
Oy	81	TyrAsnValLeuGluArgProArgGlyTTPalaPheIleTyrHisAlaPheValPheLeu	100
Db	250	TACACGCTCTGGAGAGACCCCGCGCTGGCGCTTCATCTACACACGCTTCGTTTTCTC	309
Oy	101	LeuValPheGlyCysIleuIleLeuSerValPheSerThrIleProGluHisThrLysLeu	120
Db	310	CTTGCTTTGGTGGCTTGATATTTGTAGCTTTTCTACCATTCCTGTAGCACACAAAATTTG	369
Oy	121	AlaSerSerCysLeuLeuIleLeuGluPheValMetIleValPheGlyLeuGluPhe	140
Db	370	GGCTCAAGTGGCTCTTGATMCCGAGAGTGTGATATGTTCTGCTTTGGTTGGAGTTC	429
Oy	141	IleIleArgIleTyrSerAlaGlyCysCysArgTyrArgGlyTyrPngIleYargLeu	160
Db	430	ATCATTCGATMCTGGCTCGCGGCTTCTGTTGCGATATAGAGATGGCAAGAACTCG	489
Oy	161	ArgPheAlaArgLysProPheCysValIleAspThrIleValIleAlaSerIleAla	180
Db	490	AGGTTTGGTCGAAAGCCCTTGCTGTATAGATACCAATTTCTTACCGCTCAATAGCA	549
Oy	181	ValValSerAlaLysThrGlnGlyAsnIlePheAlaThrSerAlaLeuArgSerLeuArg	200
Db	550	GTTGTTTTCGCAAAAACCTAGGTAATATTTTGGCCACGTCGTGCACTCAGAGTCTCGT	609
Oy	201	PheLeuGlnIleLeuArgMetValArgMetAspArgArgGlyLysThrTyrLysLeuLeu	220
Db	610	TTCTCAACAGATCCTCCGCAATGCGGCATGAGACCAAGGAGGACCTTGGAAATTACTG	669
Oy	221	GlySerValValTyrAlaHisSerLysGluLeuIleThrAlaTyrTyrIleGlyPheLeu	240
Db	670	GGTCAGTGGTTATGCTCCACACCAAGAAATTAATCACACCTGGTCAATAGATTTTTTG	729
Oy	241	ValLeuIlePheSerSerPheLeuValTyrLeuValGluLysAspAlaAsnLysGluPhe	260
Db	730	GTTCTTATTTTTCGCTTTCTCTTCTATCTGCTGAAAAAGATGCCAATAAGACTTT	789
Oy	261	SerThrTyrAlaAspAlaLeuTrrPrgIyThrIleThrLeuThrThrIleGlyTyrGly	280
Db	790	TCTACATATGCAAGATGCTCTGCTGGGGCACAATTGACATGCAACTATTCCTATGGA	849
Oy	281	AspLysThrProLeuThrTrpLeuGlyArgLeuLeuSerAlaGlyPheAlaLeuLeuGly	300
Db	850	GACAAACCTCCCTAATCTGGCGGGAAGATTTCTTCTCAGGCTTGGACCTCCCTGGC	909
Oy	301	IleSerPhePheAlaLeuProAlaGlyIleLeuGlySerGlyPheAlaLeuLysValGln	320
Db	910	ATTTCTTTTTCGACTTCTCTCGCGGCATTTCTTGCTCAGGTTTGGATTAAGTACAA	969
Oy	321	GluGlnHisArgGlnLysHisPheGluLysArgArgAsnProAlaAlaAsnLeuIleGln	340
Db	970	GAACAACACCGCCAGAAACACTTGAAGAAAGAAAGAACCCAGCTGCCAACCCTATTCAG	1029
Oy	341	CysValTrrPargSerTyrAlaAlaAspGluLysSerValSerIleAlaThrTrrLysPro	360
Db	1030	TGTGTTGGCGTAGTACCCAGCTGATGAAGAAATCTGTTCCATTGCCAACCTGGAAGCA	1089
Oy	361	HisLeuLysAlaLeuHisThrCysSerProThr-----	371
Db	1090	CACTTGAGAGCCCTTGCACACCTGCACCCCTACCAAGAAACAAGGGGAAGCATCAAGC	1149
Oy	372	AsnGlnLysLeuSerPheLysGluArgValArgMetAlaSerProArgGlyGlnSerIle	391
Db	1150	ACTCAGAACTAAGTTTAAAGAGGACAGTCCGATGCTAGCCCGCAGGGCCCAAGATATT	1209
Oy	392	LysSerArgGlnAlaSerValGlyAspArgArgSerProSerThrAspIleThrAlaGlu	411
Db	1210	AAGAGCGGCAAGACCTCAGTAGTGTGACAGAGGTGCCCAAGCACCGCATCACAGCGAG	1269

QY	412	GlySerProThrLysValGlnLysSerThrPserPheAsnAspArgThrArgPheArgPro	431
Db	1270	GCCAGTCCCAACCAAGTGGAGAAAGCTGGAGACTTCAACGACCGAACCCGCTTCGGGCC	1329
QY	432	SerLeuArgLeuLysSerSerGlnProIleProIleValIleAspAlaSerThrAlaLeuGly	451
Db	1330	TGGCTGGCGCTCAAAAGTTCTCAGCCAAACCGATGATGATGCTGACACACGCCCTTGGC	1389
QY	452	ThrAspAspValTyrAspGlnLysGlyGlyGlnCysAspValSerValGlnAspLeuThr	471
Db	1390	ACTGATGATGCTATATGATGATGAAAGATGCGCAGTGTGTATCTAGTGGAGACCTCAC	1449
QY	472	ProProLeuLysThrValIleArgAlaIleArgIleMetLysPheHisValAlaLysArg	491
Db	1450	CCACACCTTAAACGTCATCTTGACCTTCACAAAATTATGAATTTTCATGTTGCCAAACGG	1509
QY	492	LysPheLysGlnThrLeuArgProTyrArgAspValLysAspValIleGlnGlnTyrSerAla	511
Db	1510	AAGTTTAAAGGAACACCTTACCTCCATATGATGTGAAGATGTCATTTGAACCAATATTCTGCT	1569
QY	512	GlyHisLysAspMetLeuCysArgIleLysSerLeuGlnThrArgValAspGlnIleLeu	531
Db	1570	GCTCATCTCGACATGTGTGTGATTTAAAGCCCTTCAACACGCTTGATCAAAATCTT	1629
QY	532	GlyLysGlnGlnIleThrSerArgLysLysSerArgGlyLysIleThrAlaGlnHisGln	551
Db	1630	GGAAAAAGGCCAATCATCATCATGAATGAAGAGCCGAGAGAAATATACAGCGAACAATAG	1689
QY	552	ThrThrAspAspLysSerMetLeuGlnTyrArgValLysValGlnLysGlnValGlnSer	571
Db	1690	ACCACAGACGATCTCAGTATGCTCGTGGCGGTGCACAGGTTGAAGAAACAGTACAGTCC	1749
QY	572	IleGlnSerLysLeuAspCysLeuLeuAspIleTyrGlnGlnValLeuArgLysLysSer	591
Db	1750	ATAGATATCCAACTGGACGCTCTACTGAACATCTATCAACAGCTCTTCGGAAAGCTCT	1809
QY	592	AlaSerAlaLeuAlaLeuAlaSerPheGlnIleProProPheGlnLysGlnGlnThrSer	611
Db	1810	GGCTACGCCCTGGCTTGGCTTCATTTCCAGTTCGCCACCTTTTGATGTGAACAGACATCT	1869
QY	612	AspTyrGlnSerProValAspSerLysAspLeuSerGlySerAlaGlnAsnSerGlyCys	631
Db	1870	GACTATCAAAAGCCCTGTGATGAGCAAAATCTTTGGGTTCGGCAAAACAGTGGCTGC	1929
QY	632	LeuSerArgSerThrSerAlaAsnLysSerArgGlyLeuGlnPheIleLeuThrProAsn	651
Db	1930	TTATCCAGATCAACTAGTGGCACAATCTTCGAGAGGCTCGAATTATTTCTGACGCCAAT	1989
QY	652	GluPheSerAlaGlnThrPheTyrAlaLeuSerProThrMetHisSerGlnAlaThrGln	671
Db	1990	GAGTTCAGGCCCAACACTTCTTACCCGCTTACCTACTATGCACAGTCAAGCAACACAG	2049
QY	672	ValProLysSerGlnSerAspGlySerLysAlaValAlaIleThrAsnThrIleAlaAsnGln	691
Db	2050	GTGCCAATTAGTCAAAAGCGATGGCTGAGAGTGGGAGCCACCAACCAATTTGCAACCA	2109
QY	692	IleAsnThrAlaProLysProAlaIleProThrThrLeuGlnIleProProProLeuPro	711
Db	2110	ATAAATACGGCACCCAAAGCCACAGCCCAACACTTTACAGATCCCACTCTCTCCCA	2169
QY	712	AlaIleLysHisLeuProArgProGlnThrLeuHisProAsnProAlaGlyLeuGlnGln	731
Db	2170	GGCATTCACCACTCTCCACGGCCAAAACTGTGCACCCCTTAACCTCGAGGCTTACAGAA	2229
QY	732	SerIleSerAspValThrThrCysLeuValAlaSerLysGlnAsnValGlnValAlaGln	751
Db	2230	ACGATTTTCGAGCTACCAACCTGCTGTGGCTGCCCAAGAAATGTTCCAGTTGCCACAG	2289
QY	752	SerAsnLeuThrLysAspArgSerMetArgLysSerPheAspMetGlyGlyGlnThrLeu	771
Db	2290	TCTAATCTTCACCAAGACCGTTCTGTGAGAAACCTTTGACATGGGAGGAACACTGTG	2349

QY 772 LeuSerValCysProMetValProLysAspLeuGlyLysSerLeuSerValGlnAsnLeu 791
 |||||||
 Db 2350 TTGTGTGTGTGTCATGGTGGCGAAGACTGGCAATCTTGTGTGTGCAAAACCTG 2409
 QY 792 IleArgSerThrGluGlnLeuAsnIleGlnLeuSerGlySerGlnSerGlySerArg 811
 |||||||
 Db 2410 ATCAGGTGACCGAGAACTGATATACAACTTTCAGGGAGTGAATCAAGTGCCTCCAGA 2469
 QY 812 GlySerGlnAspPheThrProLysThrPargGlnSerLysLeuPheIleThrAspGln 831
 |||||||
 Db 2470 GGCACCCAGATTTTATCCCAATGAGGAAATCCAAATGTTTATTAATGATGAAGAG 2529
 QY 832 ValGlyProGluGlnThrGlnThrAspThrPheAspAlaAlaProGlnProAlaArgGlu 851
 |||||||
 Db 2530 GTGGGTCCCGAAGACAGACAGACACTTTGTGATGCCGACCGAGCTGCCAGGGA 2589
 QY 852 AlaAlaPheAlaSerAspSerLeuArgThrGlyArgSerArgSerGlnSerIleCys 871
 |||||||
 Db 2590 GCTGCTTTCATCAGACTCTAAGAGCTGAGAGGTCAAGATCATCTCAGACATTTGT 2649
 QY 872 LysAlaGlyGlnSerThrAspAlaLeuSerLeuProHisValLysLeuLys 888
 |||||||
 Db 2650 AAGCAGGAGAAATGATGATGCCCTGACCTTGCATGTCATAACTGAAA 2700
 RESULT 8
 ID AAH49499 standard; DNA; 3074 BP.
 XX
 AC AAH49499;
 XX
 DT 11-DEC-2001 (first entry)
 XX
 DE Human KCNQ5 DNA.
 XX
 KW KCNQ5; potassium channel protein; human; neurological; cardiovascular;
 KW anticonvulsant; excitability modulator; membrane potential; neuron;
 KW voltage-dependent; KCNQ5 potassium channel; cardiomyocyte; epilepsy;
 KW screening; central nervous system disease; cardiovascular disease; ds.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 110..2908
 FT /*tag= a
 FT /product= "KCNQ5"
 XX
 PN DE10013732-A1.
 XX
 XX 27-SEP-2001.
 PD
 XX 21-MAR-2000; 2000DE-1013732.
 PF
 XX 21-MAR-2000; 2000DE-1013732.
 PR
 XX (AVET) AVENTIS PHARMA DEUT GMBH.
 PA
 PI Steinmeyer K, Lerche C, Scherer C, Seeborn G, Busch AE.
 PI WPL: 2001-571700/65.
 DR P-PSDB: AAB86979.
 DR
 XX
 PT New DNA sequence encoding potassium channel KCNQ5, useful in screening
 PT for specific modulators, potential agents for treating central nervous
 PT system and cardiovascular diseases
 PT
 PS Claim 2a; Page 9-10; 20pp; German.
 XX
 CC This invention describes a novel DNA sequence (I) encoding: (i) a
 CC polypeptide (II) with potassium channel KCNQ5 activity; (ii) a
 CC polypeptide with the amino acid (aa) sequence of KCNQ5. The products of
 CC the invention have neurological, cardiovascular and anticonvulsant
 CC activity and act as modulators of the voltage-dependent KCNQ5 potassium
 CC channel, a key regulator of membrane potential and modulator of

CC excitability of electrically activated cells such as neurons and
 CC cardiomyocytes. KCNQ5 may be implicated in some forms of epilepsy. (II)
 CC are used to screen for compounds that modulate the activity of KCNQ5,
 CC potentially useful for treating central nervous system (e.g. epilepsy)
 CC and cardiovascular diseases. This sequence encodes the human
 CC potassium channel KCNQ5 protein described in the invention.
 XX
 SQ Sequence 3074 BP; 788 A; 784 C; 789 G; 713 T; 0 other:
 Alignment Scores:
 Pred. No.: 0 Length: 3074
 Score: 4513.50 Matches: 885
 Percent Similarity: 98.77% Conserved: 1
 Best local Similarity: 98.66% Mismatches: 2
 Query Match: 99.26% Indels: 9
 DB: 22 Gaps: 1
 US-09-810-796-5 (1-888) x AAH49499 (1-3074)
 QY 1 MetLysAspValGlnSerGlyArgGlyValLeuAsnSerAlaAlaArgGly 20
 |||||||
 Db 215 ATGAAGGATGTGAGTCCGGCCGAGGAGGTCTGCTGAACCTGGCAGCCGAGGGGC 274
 QY 21 AspGlyLeuLeuLeuGlnGlyThrArgAlaAlaThrLeuGlyGlyGlyGlyLeu 40
 |||||||
 Db 275 GACGGCTGTACTGTGGCCAGCCCGCGGCGACGCTTGTTGGGGGGGGGGCTG 334
 QY 41 ArgGlnSerArgArgGlyLysGlnGlyAlaArgMetSerLeuLeuGlyLysProLeuSer 60
 |||||||
 Db 335 AGGAGAGACCCCGCGGACAGCGGCGCGGATGAGCTGCTGGAAAGCCCGCTCT 394
 QY 61 TyrThrSerSerGlnSerCysArgArgAsnValLysTyrArgArgValGlnAsnTyrLeu 80
 |||||||
 Db 395 TACACGACTACCCAGAGCTGCCGGCGCAACGTCAAGTACCGGGGTGAGAACTACTG 454
 QY 81 TyrAsnValLeuGlnArgProArgProArgGlyTyrAlaPheIleTyrHisAlaPheValPheLeu 100
 |||||||
 Db 455 TACAACGCTGAGAGACAGCCCGCGGCTGGGGCTCATCTACACGCTTCTTCTTC 514
 QY 101 LeuValPheGlyCysLeuIleLeuSerValPheSerThrIleProGlnHisThrLysLeu 120
 |||||||
 Db 515 CTTCCTTTGGTCTGATTTGTCAGTGTGTTTCTACCATCCCGACACCAAAATG 574
 QY 121 AlaSerSerCysLeuLeuIleLeuGlnPheValMetIleValIlePheGlnGlnPhe 140
 |||||||
 Db 575 GCCTCAAGTCCCTCTTATCTCTGAGTTCTGATGATTTGCTTGTGGTGGATTC 634
 QY 141 IleIleArgIleTyrSerAlaGlyCysCysArgTyrArgGlyTyrPoleGlnArgLeu 160
 |||||||
 Db 635 ATCATTTGAACTGTGTTGCGGGTGTCTGTTGTCATATAGAGATGGCAAGAGACTG 694
 QY 161 ArgPheAlaArgLysProPheCysValIleAspThrIleValLeuIleAlaSerIleAla 180
 |||||||
 Db 695 AGGTTTGCTCGAAAGCCCTCTGTTGTATAGTACCATTTGCTTATGCTTCAATAGCA 754
 QY 181 ValValSerAlaLysThrGlnGlyAsnIlePheAlaThrSerAlaLeuArgSerLeuArg 200
 |||||||
 Db 755 GTTGTTCGCAAAACTCAGGGTAATATTTTGGCAGCTGCACTAGAGTCTCCGT 814
 QY 201 PheLeuGlnIleLeuArgMetValArgMetAspArgGlyGlyThrTyrLysLeuLeu 220
 |||||||
 Db 815 TTCTTACAGATCCCTCCGATGCTGGCGCATGAGCCGAAGGGAGGAGCTGGAATTACG 874
 QY 221 GlySerValValTyrAlaHisSerLysGlnLeuIleThrAlaTyrTyrIleGlyPheLeu 240
 |||||||
 Db 875 GTTCAGTGTGTATGTCACACAGCAAGAAATTAACACAGCTGTGATAGATTGTTG 934
 QY 241 ValLeuIlePheSerSerPheLeuValTyrLeuValGluLysAspAlaAsnLysGluPhe 260
 |||||||
 Db 935 GTTGTATTTTTCCTCTTCTGCTATCTGTGGGAAAGAGATCAATTAAGAGTTT 994
 QY 261 SerThrTyrAlaAspAlaLeuTyrProGlyThrIleThrLeuThrThrIleGlyGly 280
 |||||||

Db 995 TCATCATATGACAGATGCTCTGTGGGGGCACAAATTACATTGCACAACATATTGGCTATGCA 1054
 Oy 281 AsplystrProleuthrTripleuGlyVarpleuSerIaGlyPheAlaLeuengly 300
 Db 1055 GACAAATCTCCCTTAACCTTGGCTGGGAAGATTGCTTTCTGCAGGCTTTGGCACTCTCTGGC 1114
 Oy 301 IleSerPhePheAlaLeuProAlaGlyIleLeuGlySerGlyPheAlaLeuLysValGln 320
 Db 1115 ATTCTTCTTCTTGGCACTTCCCTGGCGGCACTTCTGGCTCAGGTTTGCATTAAATACAA 1174
 Oy 321 GluGlnHisAlaGlnLysHisPheGlnLysArgArgAsnProAlaAlaAsnLeuIleGln 340
 Db 1175 GAACAACACCCCGCAAAACCTTTGAGAAAGAAAGAACCCAGCTGCCAACCTCATTTAG 1234
 Oy 341 CysValTrpArgSerTyrAlaAlaAspGlnLysSerValSerIleAlaThrTrpLysPro 360
 Db 1235 TGTGTTTGGCTAGTACCGACGCTGATGAGAAATCTGTTTCATTGCCAACCTGGAAAGCA 1294
 Oy 361 HisLeuLysAlaLeuHisThrCysSerProThr 371
 Db 1295 CACTTGAAGGCTTGGACACCTGCAGCCCTACCAAGAAAGAAAGAGGGAAGCATCAAGC 1354
 Oy 372 AsnGlnLysLeuSerPheLysGlnArgValArgMetAlaSerProArgGlyIleSerIle 391
 Db 1355 AGTCAGAGCTAACGTTTAAAGAGAGAGTGGCAGCTAGCCCGGAGGCGGAGATATT 1414
 Oy 392 LysSerArgGlnAlaSerValGlyAspArgArgSerProSerThrAspIleThrIleGln 411
 Db 1415 AAGAGCCGACAAAGCTCAGTAGTGACAGAGGTCCCAAGCACCAGACATCCACACCCGAG 1474
 Oy 412 GlySerProThrLysValGlnLysSerTrpSerPheAsnAspArgThrArgPheArgPro 431
 Db 1475 GGCAGTCCACCAAGAGTGCAGAGCTGAGCTTCAACGACCGAACCCGCTCCGGGCC 1534
 Oy 432 SerLeuArgLeuLysSerSerGlnProLysProValIleAspAlaAspThrAlaLeuGly 451
 Db 1535 TCGCTGGCCCTCAAAAGTTCTCAGCCAAACAGATGATAGTGCAGACAGCCCTTGCC 1594
 Oy 452 ThrAspAspValTyrAspGlnLysGlyCysGlnCysAspValSerValGlnAspLeuThr 471
 Db 1595 ACTGATGATGATATGATGAGAAAGAGATGCCAGTGTGATGATACGTGGAGACCTCACC 1654
 Oy 472 ProProleuLysThrValIleArgAlaIleArgIleMetLysPheHisValAlaLysArg 491
 Db 1655 CCACCCTAAACCTGTCATTCAGAGCTATCAGAAATTATGAATTTTCATGTCAGAAACGG 1714
 Oy 492 LysPheLysGlnThrLeuArgProThrLysValLysAspValIleGlnGlnTyrSerAla 511
 Db 1715 AAGTTTAAAGAAACATTAAGTCCATATGATGATAAAGATGTCATTGAACAAATATTCTGCT 1774
 Oy 512 GlyHisLeuAspMetLeuCysArgIleLysSerLeuGlnThrArgValAspGlnIleLeu 531
 Db 1775 GGTGATCTGGAGCATGTTGTGTAGAAATTAAAGCCCTTCAACACGCTGTTGATCAAAATTCTT 1834
 Oy 532 GlyLysGlnGlnIleThrSerAspLysLysSerArgGlnLysIleThrAlaGlnHisGln 551
 Db 1835 GGAAGAGGGCAAAATCAGATCAGATAAGAGAGCCGAGAGAAATTAACAGCAGAACATGAG 1894
 Oy 552 ThrThrAspAspLeuSerMetLeuGlyArgValLysValGlnLysGlnValGlnSer 571
 Db 1895 ACCCAGACGATCTCAGATGCTGGTGGGTGTCAGAGTTTGAAAACACAGTAAAGTCC 1954
 Oy 572 IleGlnSerLysLeuAspCysLeuLeuAspIleTyrGlnGlnValLeuArgLysGlySer 591
 Db 1955 ATAAATTCAGAGCTGAGCTGCTACTAGACATCTATCAACAGGTCTCTCGGAAAGGCTCT 2014
 Oy 592 AlaSerAlaLeuAlaLeuAlaSerPheGlnIleProProPheGlnCysGlnGlnThrSer 611
 Db 2015 GCCTCAGGCCCTCGCTTGGCTTCATTCAGATCCACACTTTGGAATGGAACACAGCATCT 2074
 Oy 612 AsplyrGlnSerProValAspSerLysAspLeuSerGlySerAlaGlnAsnSerClyLys 631
 Db 2075 GACTATCAAAAGCCCTGTGGATGAGCAAGATCTTTTCCGGGTTCCGACAAACAGTGGCTGC 2134

Oy 632 LeuSerArgSerThrSerAlaAsnIleSerArgGlyLeuGlnPheIleLeuThrProAsn 651
 Db 2135 TTATCCAGATTCACATAGTGCACACATCTGCAGAGGCCCTGCAGTTCTTGCAGCCCAAT 2194
 Oy 652 GluPheSerAlaGlnThrPheTyrAlaLeuSerProThrMetHisSerGlnAlaThrGln 671
 Db 2195 GAGTTCAGTGGCCAGACTTCTTACGGCGCTTACGCCCTACTATGCACAGTCACAGCAACAG 2254
 Oy 672 ValProIleSerGlnSerAspGlySerAlaValAlaIleThrAsnThrIleAlaAsnGln 691
 Db 2255 GTGCCAATTAGTCAAAAGCGATGCTCAGCAGTGCAGCCACCAACACCATTCGCAACCA 2314
 Oy 692 IleAsnThrAlaProLysProAlaIleProThrThrLeuGlnIleProProProLeuPro 711
 Db 2315 ATAAATTCAGCAGCCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 2374
 Oy 712 AlaIleLysHisLeuProArgProGlnThrLeuHisProAsnProAlaGlyLeuGlnGln 731
 Db 2375 GCCATCAAGCATCTGCCAGGCCAGAACTCTGCACCCCTAACCTGCAAGGCTTACAGGAA 2434
 Oy 732 SerIleSerAspValThrThrCysLeuValAlaSerLysGlnAsnValGlnValAlaGln 751
 Db 2435 ACCATTCTGACAGTCAACGACCTGCTTGTGGCTCCCAAGGAAATGTTCCAGGTTGCACAG 2494
 Oy 752 SerAsnLeuThrLysAspArgSerMetArgLysSerPheAspMetGlyValGlnThrLeu 771
 Db 2495 TCAATTCACCAAGACCCGCTCTATGAGGAAAGAGCTTTGACATGAGGAGAGAAACTG 2554
 Oy 772 LeuSerValCysProMetValProLysAspLeuGlyLysSerLeuSerValGlnAsnLeu 791
 Db 2555 TTGCTGTGTCGCCATGGTGGCCGAAGACTTGGGCAAACTTTTGTGTCGCAAAACCTG 2614
 Oy 792 IleArgSerThrGlnGlnLeuAsnIleGlnLeuSerGlySerGlnSerSerGlySerArg 811
 Db 2615 ATCAGAGTCAGCCGAGAGACTGATATACAACTTTCAGGAGAGAGATCAAGTGGCTCCAGA 2674
 Oy 812 GlySerGlnAspPheTyrProLysTrpArgGlnSerLysLeuPheIleThrAspGlnGln 831
 Db 2675 GGCAGCCAAAGATTTTACCACCCAATGAGAGGAAATCCAAATTTTATATACGTATGAGAG 2734
 Oy 832 ValGlyProGlnGlnThrGlnThrAspThrPheAspAlaAlaProGlnProAlaArgGln 851
 Db 2735 GTGGTCCCGAAGAGACAGACACACTTTTGTATGTCGCGCACCCAGCCTGCCAGGAA 2794
 Oy 852 AlaAlaPheAlaSerAspSerLeuArgThrGlyArgSerArgSerSerGlnSerIleCys 871
 Db 2795 GCTGCCCTTGCATCAGACTCTCTAAGAGACTGGAAGTCAACGATCATCTCAGAGCATTTGT 2854
 Oy 872 LysAlaGlyGlnSerThrAspAlaLeuSerLeuProHisValLysLeuLys 888
 Db 2855 AAGCAGCAGGAAGATACAGATGCTCCCTCACTGCTCCTCATGTCAAACTGAA 2905
 RESULT 9
 AAC64371
 ID AAC64371 standard: cDNA: 3718 BP.
 AC AAC64371:
 XX 07-FEB-2001 (first entry)
 DT
 XX
 DE Human KCNQ5 (KCN6q) cDNA sequence SEQ ID NO:2.
 XX
 KW Human; KCNQ5; KCN6q; chromosome 6; voltage-gated potassium channel;
 KW Stargardt-like macular dystrophy; cone-rod macular dystrophy;
 KW Salla disease; ophthalmological; auditory; central nervous system;
 KW cardiocative; anticonvulsant; gastrointestinal; muscular active;
 KW age-related macular degeneration; macular degeneration; deafness;
 KW epilepsy; neuropsychiatric disorder; heart disorder; muscle disorder;
 KW gastrointestinal disorder; ss.
 XX
 OS Homo sapiens.
 XX

QY 528 AspGlnIleLeuGlyLysGlyGlnIleThrSerAspLysLysSerArgLysIleThr 547
 |||
 |||
 Db 1593 GATCAATCTTGGAAAAAGGCAATCATCATAGATAAGAGAGCCGAGAAATATACA 1652
 QY 548 AlaGluHisIleThrThrAspAspLeuSerMetLeuGlyArgValValLysValLys 567
 |||
 |||
 Db 1653 GCAGAACATGAGACACAGAGATCTGATGCTGGTGGGAGTCAAGCTGAAAAA 1712
 QY 568 GluValGlnSerIleGlnSerLysLeuAspCysLeuLeuAspIleTyrGlnGlnValLeu 587
 |||
 |||
 Db 1713 CAGGTACAGTCCATAGATATCCAGCTGACTGCTACTAGACATCTATCAACAGGCTCTT 1772
 QY 588 ArgLysGlySerAlaSerAlaLeuAlaLeuAlaSerPheGlnIleProPheGlnCys 607
 |||
 |||
 Db 1773 CGGAAAGGCTCTGCTCAGCCCTGCTTGGCTTCATTCAGATCCACCTTTGAATGT 1832
 QY 608 GluGlnThrSerAspTyrGlnSerProValAspSerLysAspLeuSerGlySerAlaGln 627
 |||
 |||
 Db 1833 GAACAGACATCTACTATTCAAAGCCCTGTGATAGCAAAAGATCTTTCGGTTCGCCACAA 1892
 QY 628 AsnSerGlyCysLeuSerArgSerThrSerAlaAsnIleSerArgGlyLeuGlnPheIle 647
 |||
 |||
 Db 1893 AACAGTGGCTGCTTATTCACATCATCTAGTCCAAACATCTCGAGAGGCTCGAGTTCATT 1952
 QY 648 LeuThrProAsnGluPheSerAlaGlnThrPheTyrAlaLeuSerProThrMetHisSer 667
 |||
 |||
 Db 1953 CTGACGCCAATAGTTCAGTTCAGTCCAGACTTTCACGGGCTTAGCCCTACTATGACAGT 2012
 QY 668 GlnAlaThrIleValProIleSerGlnSerAspGlySerAlaValAlaIleThrAsnThr 687
 |||
 |||
 Db 2013 CAAGCAACACAGGTCCTCAATTAGTCAAAAGCATGCTCAGCAGTGGCAGCCACCAACACC 2072
 QY 688 IleAlaAsnGlnIleAsnThrAlaProLysProAlaIleProThrLeuGlnIlePro 707
 |||
 |||
 Db 2073 ATTGCAAACCAATTAATACGGCACCACAGCCAGACGCCCAACACTTTCAGATGCCCA 2132
 QY 708 ProProLeuProAlaIleLysHisLeuProArgProGluThrLeuHisProAsnProAla 727
 |||
 |||
 Db 2133 CCTCCTCTCCACCATCATGATCTGCCAGGCCAGAACTTCGACCTTAACCTTCA 2192
 QY 728 GlyLeuGlnGlnSerIleSerAspValThrThrCysLeuValAlaSerLysGlnAsnVal 747
 |||
 |||
 Db 2193 GGGCTTACAGAAAGCATTTCTGACGTCCACACCTGCTTGGCTCCCAAGAAATGT 2252
 QY 748 GlnValAlaGlnSerAsnLeuThrLysAspArgSerMetArgLysSerPheAspMetGly 767
 |||
 |||
 Db 2253 CAGGTTCACAGTCAATCTCACCAAGAGCCGTTCTATGAGAAAGCTTTGACATGGGA 2312
 QY 768 GlyGluThrLeuLeuSerValCysProMetValProLysAspLeuGlyLysSerLeuSer 787
 |||
 |||
 Db 2313 GGAGAAACTCTGTGCTCTCTGCTCCATGGTGGCCGAAGCACTTGGCAAAATCTTGTCT 2372
 QY 788 ValGlnAsnLeuIleArgSerThrGluGluLeuAsnIleGlnLeuSerGlySerLeuSer 807
 |||
 |||
 Db 2373 GTGCAAAACCTGATCAGGTGACCGAGGAAGTGAATATACACTTTCAGGAGTGAGTCA 2432
 QY 808 SerGlySerArgLysSerGlnAspPheTyrProLysTyrArgGlnSerLysLeuPheIle 827
 |||
 |||
 Db 2433 AGTGCTCCAGAGGAGCCAAAGATTTTACCCCAATGAGAGGAATCCAAATTTGTTATA 2492
 QY 828 ThrAspGlnGluValGlyProGluGluThrGluThrAspThrPheAspAlaAlaProGln 847
 |||
 |||
 Db 2493 ACTGATGAAGAGGTGGTCCCGAAGACAGACAGACACTTTTATGCGCCAGACCCGAG 2552
 QY 848 ProAlaArgGluAlaAlaPheAlaSerAspSerLeuArgThrGlyArgSerArgSerSer 867
 |||
 |||
 Db 2553 CCGGCAAGGAGAACTGCTTGCATCAGACTCTTAAGAGCTGAAGGTGACAGATCACT 2612
 QY 868 GlnSerIleCysLysAlaGlyGlnSerThrAspAlaLeuSerLeuProHisValLysLeu 887
 |||
 |||
 Db 2613 CAAGAGCATTTGTAAGGACGAGGAAGATACAGATGCCCTACACTTGCCTCATGTCAAACTG 2672
 QY 888 Lys 888

Db 2673 AAA 2675
 |||
 RESULT 10
 ID AAA47618
 AC AAA47618;
 XX 08-NOV-2000 (first entry)
 DE KCNQ4 Potassium channel gene.
 XX
 XX KCNQ4: potassium channel; cardiac arrhythmia; neonatal epilepsy;
 KW deafness; probes; treatment; therapy; transgenic animal; antibody;
 KW agonist; antagonist; tinnitus; hearing loss; neonatal deafness;
 KW presbycusis; affective disorder; compulsive behavior; dementia;
 KW ataxia; cognitive deficits; Huntington's disease; mania; memory impairment;
 KW depression; neurodegenerative disease; Parkinson's disease;
 KW motor disorders; psychosts; schizophrenia; spinal cord damage;
 KW Pick's disease; stroke; tremor; ds.
 KW
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 83..2170 /tag_a
 FT /product= KCNQ4 Potassium channel polypeptide
 FT
 PN WO200044786-A1.
 XX
 PD 03-AUG-2000.
 XX
 PE 19-JAN-2000; 2000MO-DK00024.
 XX
 PR 26-JAN-1999; 99DK-0000076.
 PR 19-MAY-1999; 99DK-0000693.
 XX
 PA (NEUR-) NEUROSEARCH AS.
 XX
 PI Jentsch TJ;
 XX
 DR P-PSDB; AAB01476.
 XX
 PT Nucleic acids encoding the novel KCNQ4 potassium channel subunit,
 PT useful e.g. for treating tinnitus, deafness, Alzheimer's and
 PS Parkinson's diseases
 PS
 XX
 Claim 1; Page 43-48; 65pp; English.
 CC Mutations in 3 known genes of the KCNQ branch of the potassium
 CC channel gene family underlie inherited cardiac arrhythmia's, neonatal
 CC epilepsy and in some cases associated with deafness. KCNQ4 has been
 CC mapped to the DFNA2 locus for autosomal dominant hearing loss, and
 CC a dominant negative KCNQ4 mutation that causes deafness in a DFNA2
 CC pedigree has been identified. KCNQ4 is the first potassium channel
 CC gene underlying non-syndromic deafness. KCNQ4 forms heteromeric
 CC channels with other KCNQ channel subunits, especially KCNQ3.
 CC Nucleotides encoding the KCNQ4 protein and the protein itself may be
 CC used in the prevention, treatment and diagnosis of diseases
 CC associated with inappropriate KCNQ4 expression. The nucleotides may
 CC also be used as DNA probes in diagnostic assays (e.g. polymerase
 CC chain reactions (PCR)) to detect and quantitate the presence of
 CC similar nucleic acid sequences in samples and to identify mutations
 CC within them, and hence which patients may be in need of restorative
 CC therapy. They may also be used to study the expression and function
 CC of KCNQ4 polypeptides and their role in metabolism, for example
 CC through the production of transgenic animals. The KCNQ4 polypeptides
 CC may be used as antigens in the production of antibodies and to
 CC identify modulators (agonists and antagonists) of KCNQ4 expression
 CC and activity. The anti-KCNQ4 antibodies and KCNQ4 antagonists may

CC also be used to down regulate KCNQ4 expression and activity. They may
CC be used in this way to treat tinnitus, loss of hearing (especially
CC progressive hearing loss, neonatal deafness and presbycusis
CC (deafness of the elderly)) and disease or adverse conditions of the
CC central nervous system (CNS) such as affective disorder, Alzheimer's
CC disease, anxiety, ataxia, CNS damage caused by trauma, stroke or
CC neurodegenerative illness, cognitive deficits, compulsive behavior,
CC dementia, depression, Huntington's disease, mania, memory impairment,
CC memory disorders and dysfunctions, motion disorders, motor disorders,
CC neurodegenerative diseases, Parkinson's disease, Parkinson-like motor
CC disorders, phobias, Pick's disease, psychosis, schizophrenia, spinal
CC cord damage, stroke and/or tremor. Conversely, antisense nucleic acid
CC molecules may be administered to down regulate KCNQ4 expression by
CC binding with the cells own KCNQ4 genes and preventing their
CC expression.

XX Sequence 2335 BP; 396 A; 812 C; 719 G; 408 T; 0 other;

Alignment Scores:

Pred. No.:	1-766-161	Length:	2335
Score:	2007.50	Matches:	434
Percent Similarity:	65.32%	Conservative:	82
Best Local Similarity:	54.94%	Mismatches:	133
Query Match:	44.15%	Indels:	141
DB:	21	Gaps:	16

US-09-810-796-5 (1-888) x AAA47618 (1-2335)

QY 8 ArgGlyArgValLeuLeuAsnSerAlaAlaAlaArgGlyAspGlyLeuLeuLeuGly 27
DB 127 CGGGAGACCCCGCCCGGAGCTAGTGGCTCAGCGC----- 165
QY 28 ThrArgAlaAlaThrLeuGlyGlyGlyGlyGlyLeuArgGlnSerArgArgGlyLys 47
DB 166 --GTCGAGAGCGAACAAGGCGAGCGGG-----CGGGGCGG 201
QY 48 GlnGlyAla-ArgMetSerLeuLeuGlyLysProLeu----- 59
DB 202 CTCGCCGCGCGGCTCTGCGGCTCTGCGGAGCCCCCGCGCGCGCGCCCTCCCTGG 261
QY 60 -----SerTy-TrhSerSerGlnSerCysAlaArgAsnValLysTy 73
DB 262 GCCGGGCTCCGGCTCCGCTCCGCTCCGCGGCGGCGGCTCTCCGCGCGCAAGCGCTA 321
QY 73 rArgArgValGlnAsnTyTrhLeuTrpAsnValLeuGlnArgProArgGlyTrpAlaPheI 93
DB 322 CCGCGGCTGCGAAGACTGGGTCTACACGCTGCTGGAGCGGCCCGCGGCTGGCTTCGT 361
QY 93 eTyTrhAlaPheValPheLeuLeuValPheGlyCysLeuIleLeuSerValPheSerTh 113
DB 382 CTACACGCTTCATATTGTTTGTGCTTTCAGCTGCTGCTGCTGCTGCTGCTGCTGCTG 441
QY 113 rIleProGlnHsrTrhLysLeuAlaSerSerCysLeuLeuIleLeuGlnPheValIleTil 133
DB 442 TATCCAGAGACCAACGAACTTCGCAACAGAGTGTCTCCATCTTGGAATTCCTGATGAT 501
QY 133 eValValPheGlyLeuGlnPheIleIleArgTleTrpSerAlaGlyCysCysArgTy 153
DB 502 CGTGGTTTCGGCTTGGAGTACATGCTCCGGGTCTGGTCCGGGAGTGGTGGCGGCTA 561
QY 153 rArgGlyTrpGlnGlyArgLeuArgPheAlaArgLysProPheCysValIleAspThrI 173
DB 562 CCGAGAGATGGAGGATCGCTTCGTTGGCCAGAAAGCCCTTGTGTATGACATTCAT 621
QY 173 eValIleAlaSerIleAlaValAlaSerAlaLysTrhGlnGlyAsnIlePheAlaTh 193
DB 622 CGTGTCTGGCTGCGTGGTGGCTGATCGCCGGGTACCCAGAGCAACATCTTCCACAC 681
QY 193 rSerAlaLeuArgSerLeuArgPheLeuGlnIleLeuArgMetValArgMetAspArg 213
DB 682 GTCCGCGCTGGCGACATGCTTCCTCGAGATCCCTGCGCATGGTGGATGGACCGCG 741
QY 213 gGlyGlyTrhTrpLysLeuLeuGlySerValValTrpAlaHisSerLysGlnLeuIleTh 233

DB 742 CGGGGACACCTGGAGAGCTGCGGTGCTAGTGTCTACGCGCATACAGAGACTATAC 801
QY 233 rAlaTrpTrpIleGlyPheLeuValIlePheSerSerPheLeuValTrpLeuValI 253
DB 802 CGCTGTGATCATCGGATCTCGGTCTCATCTTCCTCCCTCCGCTGCTACCTGCGCGA 861
QY 253 uLysAspAlaAsnLysGlnPheSerTrhTrpAlaAspAlaLeuTrpTrpGlyThIleTh 273
DB 862 GAAGGAGCGCAACTCCGCTTCCTCTACGCGCATCTGCTGGTGGGAGCATTTAC 921
QY 273 rLeuTrhTrhIleGlyTrpGlyAspLysTrhProLeuTrhTrpLeuGlnArgLeuLeu 293
DB 922 ATTACAAACCATCGGCTATGCTGACAAACACCGACACATGCTGGCGAGGCTCTGCG 981
QY 293 rAlaGlyPheAlaLeuLeuGlyIleSerPhePheAlaLeuProAlaGlyIleLeuGlySe 313
DB 982 TGTGGCTTCGCTTACGCGCATCTCTTCTTCTGCTGCTGCTGCGGATCTAGGCTC 1041
QY 313 rGlyPheAlaLeuLysValGlnGlnHisArgGlnLysHisPheGlnLysArgArgAs 333
DB 1042 CGGCTTGGCTTGAAGTTCAGAGACAGACCGCGGAGAACTTTCGAGAAAGCGAGAT 1101
QY 333 nProAlaAlaAsnLeuIleGlnCysValTrpArgSerTyAlaAlaAsp---GlnLysSe 352
DB 1102 GCCGGACCGCACCTCATCCAGCGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1161
QY 352 rValSerIleAlaTrp----- 358
DB 1162 CTACCTGACACCGCACCTGCTACTATGACAGTATCCCTCCATCTTCAGAGACTGCG 1221
QY 358 ----- 358
DB 1222 CTTTGTGTTGAGACGTGCACACGGGCCCGGAGGAGGCTACGGCCCTGGAGGTGCG 1281
QY 359 -----LysProHisLeuLysAlaLeuHisTh 367
DB 1282 GCGGGGCGGCTACCGACGAGACACCTCCCGTTACCGCGCGCTGGCACCTGGCACCG 1341
QY 367 r-----CysSerProTrhAsnGlnLysLeuSerPheLysGlnArgVal 381
DB 1342 GCCGGAGACACCTCTCTCTCTCTGCGGAAACGACCGCGGATGGGCATCAAGACCGCAT 1401
QY 381 rArgMetAlaSerProArgGlyGlnSerIleLysSerArgGln-----AlaSerValG 399
DB 1402 CCGCATGGGACGCTCCGAGCGGCGGAGCGGCTCTTCAAGACAGCTGGACCTTCAAC 1461
QY 399 yAspArgArgSerProSerTrhAspIleTrhAlaGlnGly---SerProTrhLysValG 418
DB 1462 AATGCCACCTCCCAAGACAGACAGTGGGTGAGGCGCACACCGCCACCAAGAGTGA 1521
QY 418 nLysSerTrpSerPheAsnAspArgTrhArgPheArgProSerLeuArgLeuLysSerSe 438
DB 1522 AAAAGAGCTGGAGCTTCATGACCGCACCGCTTCGCGGACATCTCGAAGACTC----- 1573
QY 438 rGlnProLysProValIleAspAlaAspTrhAlaLeuGlyTrhAspAspValTrpAspI 458
DB 1574 -----AAACCCCGCACCTTCTGTAAGATGCC---CCCTCAGAGGAATGACAGAGA 1623
QY 458 uLysGlyCysGlnCysAspValSerValGlnAspLeuTrhProProLeuLysThValI 478
DB 1624 GAACAGCTACACAGTGTGAGTCCAGCGGTGAGACATCATGCTGCTGTGAAGACAGTCA 1683
QY 478 eArgAlaIleArgIleMetLysPheHisValAlaLysArgLysPheLysGlnThLeuArg 498
DB 1684 CCGCTCATCGATGATTCCTCAAGTCTGCTGGTGGCCAAAAGAAATTCAGAGGAGACCTGCG 1743
QY 498 gProTyAspValLysAspValIleGlnGlnTySerAlaGlyHisLeuAspMetLeuCy 518
DB 1744 ACCGTACAGACTGAAGGACGCTATTCAGACATGACTCAGACAGCCACTGAGATCTGCG 1803
QY 518 sArgIleLysSerLeuGlnTrhArgValAlaGlnIleLeuGlnLysGlnIleThSe 538

QY 350 -----GluyservalserilealathrtrpLys----- 359
 Db 1132 TCCAGTGGCACTAGACAGGAGGTCACCGTCCAGTACAGTTCCGCAAACTCAA 1191
 QY 360 -----ProhislleuylsalaLeuHisThr----- 367
 Db 1192 ACCTACGGGGCTCCAGACTTATCCCCGCTGACACAGCTGGAGCTCTGTGAAACCTC 1251
 QY 367 ----- 367
 Db 1252 AAGATAAATCTGAGCTGCTTTACGAGAGACCCCCCGCGAGCCGCTCCAGTAA 1311
 QY 368 -----CysSerPro-----ThrAsnGlnLysLeu 375
 Db 1312 GGCAGCCCGTCAGAGAGGCCCTGTGTGATGCTGCCCGGACCGCTCTAGCCAGAAAGTTC 1371
 QY 376 SerPheylsgluarValargMetalaSerProargllyginSerlleysSerargLln 395
 Db 1372 AGTTTGAAGAATCTGTC---TTCTCAGCCCGCGAGCGCTGGCCAGAGGGAAGGGG 1428
 QY 396 AlaSerValglyasp-----ArgArgSerProserThrAspIleThrAlaGluLys 413
 Db 1429 TCCCGCAGGCCAGACTGAGCGGCTCACCCGCGCCGACAGACAGCTTCGAGAGACAGC 1488
 QY 414 ProThrLysValGlnLysSerThrPheasnAsparThrArgPheArgProSerLeu 433
 Db 1489 CCCAGCAAGGTGCCAGAGACTGAGCTTCGGGAGCCGCGGAGCCGAGCCAGGCTTTC 1548
 QY 434 ArgLeuLysSerSerGlnProLysProvalIleAspAlasphrAlaLeuGlyThrAsp 453
 Db 1549 CGCATCAAGAGGTGGCGGCTCACCGCAG-----AACTCAGAACCAAGCCCTCCCGGAGAG 1602
 QY 454 AspValThrAspGluLysGlnLysGlnCysAspValSerValGluAspLeuThrPro 473
 Db 1603 GACATTGTGATGACAAAGAGCTGCCCTCGAGTTGTGTGACGAGGAGCTGACCCGCGG 1662
 QY 474 LeuLysThrValIleargAlaIleargIleMetLysPheHisValAlaLysArgLysPhe 493
 Db 1663 CTCGAAGTGCATGACATGACAGCCGCTGTGTATGCTGCTGTCTCCAAAGCGAGATTTC 1722
 QY 494 LysGluThrLeuArgProThrAspValLysAspValIleGluGlnThrSerAlaGlyHis 513
 Db 1723 AAGGAGAGCTCGCGCCCTACGACGTGATGAGCATGTAGACAGTACAGCCGCGCCAC 1782
 QY 514 LeuAspMetLeuCysArgIleLysSerLeuGlnThrArgValAspIleLeuGlyLys 533
 Db 1783 CTGACATGCTCTCCCGAATTAGAGCTGACGTCCAGAGTGGACAGATCTGGGGCGG 1842
 QY 534 GylglnIleThrSerAspLysLysSerArgLysIleThrAlaGlnHisGluThrThr 553
 Db 1843 GGCCCGAGATCACGAGC---AAGGACCGACCAAGGCGCGCGAGCGGAGGCTGCC 1899
 QY 554 AspAspLeuSerMetLeuGlyArgValLysValLysGlnValGlnSerIleGln 573
 Db 1900 GAGGACCCACACATGATGAGCGCTCGGAAAGTGAGAAAGCAGCTCTTGCCATGGAG 1959
 QY 574 SerLysLeuAspCysLeuLeuAspIleThrGlnGlnValLeuArgLysGlySerAlaSer 593
 Db 1960 AAGAAGCTGGACTTCTCGTGAATATCTACATGAG---CGGATGGC----- 2004
 QY 594 AlaLeuAlaLeuAlaSerPheGlnIleProPheGluCys----- 607
 Db 2005 -----ATCCCCCGACAGACAGACCGAGCGCTACTTTGGGGCC 2040
 QY 608 -----GluGlnThrSerAspTyrGlnSerProValAspSerLysAspLeuSerLys 624
 Db 2041 AAGAGCCCGAGCCGGCGCGCGCTACACAGCCCGGAGACACCGGAG----- 2091
 QY 625 SerAlaGlnAsnSerGlyCysLeuSerArgSerThrSerAlaAsnIleSerArgGlyLeu 644
 Db 2092 CATGTGCAGACGACGCTCATTTGTCAAGATGCTGGCTCCAGCACTCCACGCGC--- 2148
 QY 645 GlnPheIleLeuThrProAsnGluPheSerAlaGlnThrPheTyrAlaLeuSerProThr 664

Db 2148 ----- 2148
 QY 665 MethIleSerGlnAlaThrGlnValProIleSerGlnSerAspGlySerAlaValAlaIle 684
 Db 2148 ----- 2148
 QY 685 ThrAsnThrIleAlaAsnGlnIleAsnThrAlaProLysProAlaAlaProThrThrLeu 704
 Db 2149 -----CAGAGACTTCTCGGCGCCCGCGCGCGCC---CCTGTC 2187
 QY 705 GlnIleProPro----- 2187
 Db 2188 CAGTGTCCGCTCCCTACCTCTGCGAGCCAGACACCGCGCG---CCAGGGCCACAGGAC 2246
 QY 716 LeuProArg-----ProGluThr-----LeuHis-ProAsnProAlaGlyLeuGlnG 731
 Db 2247 CTCCCGCTGGGGGACCAAGCTCTCTGTCGATCCCGCGCGCTCCCGCCAGAGCG 2306
 QY 731 uSerIleSerAspValThrThrCysLeuValAlaSerLysGlnAsnValGlnValAlaG 751
 Db 2307 GTGCTGTCCGCTACAGCGGGGCGCAACCGCGCCAGATGAGTTCTGCGGAGAGGA 2366
 QY 751 nSerAsnLeuThrLys-----AspArgSerMetArgLysSerPheAspMetGlyGly 769
 Db 2367 CACCCCGGGCTGCGAGGCCCGCCCGAGGGAGCCCTGCGGAGACAGC-----GA 2411
 QY 769 uThrLeuLeuSerValCysProMetValProLysAspLeuGlyLysSerLeuSerValG 789
 Db 2412 CAGTCCATCTCCATCCGCTCCGCTGAGCCAGAGAGAGAGAGTGGACGTTCTTCAGCGCTT 2471
 QY 789 nasnLeuIleArgSerThrGluGluLeuAsn 799
 Db 2472 CAGCATCTCCAGTCCAGAGAGAACTGAT 2502
 RESULT 13
 AAX26588
 ID AAX26588 standard; DNA; 2169 bp.
 XX
 AC AAX26588;
 XX
 DT 16-JUN-1999 (first entry)
 XX
 DE Nucleotide sequence of murine KCNQ2 (formerly known as (KvLRL).
 XX
 KW KCNQ protein; nervous system-specific potassium channel;
 KW neuronal excitability; neurotransmitter release; KCNQ modulator;
 KW ataxia; myokymia; seizure; Alzheimer's disease; Parkinson's disease;
 KW age-associated memory loss; learning deficiency; motor neuron disease;
 KW epilepsy; stroke; ss.
 XX
 OS Mus sp.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..2169
 FT CDS /*tag= a
 FN W09907832-A1.
 XX
 PD 18-FEB-1999.
 PF 26-JUN-1998; 98WO-US13276.
 PR 12-AUG-1997; 97US-0055599.
 PA (BRIM) BRISTOL-MYERS SQUIBB CO.
 XX
 PI Blazer MA, Dworetzky S, Gridkoff VK, Levesque PC;
 PI Little WA, Neubauer MG, Yang W;
 XX WPI: 1999-190047/16.
 DR P-PSDB; AAY01530.
 XX

CC human potassium channel. Antagonists can be used in modulating cognitive
CC behavioural, psychiatric, neurodegenerative and developmental disorders
CC (mental retardation) as well as asthma, migraine, epilepsy and stroke
CC and brain tumours. They can be used for treating diseases such as
CC Huntington's disease, Lou Gehrig's, neurodegeneration, multiple
CC sclerosis, psychosis, amyotrophic lateral sclerosis, retinitis
CC pigmentosa, cerebellar degeneration, urinary incontinence, diabetes,
CC asthma, premature labour, hypertension, cardiac ischemia and arrhythmias,
CC autoimmune diseases, cancer, graft rejections, acute and chronic
CC inflammation, allergies, proliferative disorders, anaemias,
CC neurodegenerative diseases with immunological components, as well as
CC autoimmune diseases including rheumatoid arthritis, type-1 diabetes
CC mellitus, myasthenia gravis, systemic lupus erythematosus, Sjogren's
CC syndrome, mixed connective tissue disease, and experimental allergic
CC encephalomyelitis (EAE).
CC
XX

SO Sequence 2565 BP; 474 A; 846 C; 818 G; 427 T; 0 other.

Alignment Scores:

Pred. No.:	8.07e-143	Length:	2565
Score:	1790.00	Matches:	411
Percent Similarity:	59.84%	Conservative:	100
Best Local Similarity:	48.13%	Mismatches:	183
Query Match:	39.37%	Indels:	161
DB:	20	Gaps:	22

US-09-810-796-5 (1-888) x AAX81548 (1-2565)

QY 17 ALaAaIarGgLyAspGlyLeuLeuLeuLeuLeuGlyThrArGAlaAaIarThrLeuGlyGly 36
Db 100 TCCACCGCGGAGCGGGCGCTGCTGATGCGCGGCTCGAGGCCCAAG-----CGC 150

QY 37 GgLyGlyGlyLeuArGgLySerArGArGgLyLysGlnGlyAlaArGwtsrLeuLeuGly 56
Db 151 GGCAGCATCTCTCAACAACCTCGCGCGGCGCGCGCGC-----GGC 195

QY 57 LysProLeuSerTrpThrSerSerGlnSerCyArGArGAsnValLysTrpArGArVal 76
Db 196 AAGCCC-----CCCAACGCGAAGCCCTTCAACGCAAGCTG 231

QY 77 GlAsnTrpTrpLeuTrpAsnValLeuGlnAlaArGArGlyTrpAlaPheLeuTrpHisAla 96
Db 232 CAGATTTCTCTTACAAACGTGGCGGCGCGCGCGCGCGCTTCATCAACAGCC 291

QY 97 PheValPheLeuLeuValPheGlyCysLeuLeuLeuSerValPheSerThrLleProGlu 116
Db 292 TAGCTGTCTCTCTGTTTTCGTCGCGTCTGCTGCTTTTCCACATCAAGAG 351

QY 117 HisTrpTrpLeuAlaSerSerCysLeuLeuLleLeuGlnPheValMetLleValValPhe 136
Db 352 TATGACAACAAGCTCGGAGGGCGCTTCAACATCTGGAATCTGTACATATGATGTTT 411

QY 137 GlyLeuGlnPheLleLleArGTrLleTrpSerAlaGlyCysCysArGTrArGlyTrp 156
Db 412 GCGGTGGATCACTTGTCGGATCGGCGCGAGGCTCTGCTCGGTAACGAGCTGG 471

QY 157 GlnGlyArGLeuArPheAlaArGTrpPheCysValLleAspThrLleValLleLle 176
Db 472 ACGGGCGGCTCAATTTGCGCGGAAACGTTGCTGTGATGATGACATCAATGAGTCTATC 531

QY 177 AlaSerLleAlaValAlaSerAlaLysThrLlnGlyAsnLlePheAlaTrpSerAlaLeu 196
Db 532 GCCTCATTTGCGGTCTGGCGCGGCTCCAGGCAACGCTTTGCGACATCTGGGCTC 591

QY 197 ArgSerLeuArGpHeLeuGlnLleLeuArGwtsrValArGwtsrAspArGArGlyTrp 216
Db 592 CGGAGCTCGCTCTCTGCGAATTTCTGGATATCCGCATGTGACCGGCGGAGGACAC 651

QY 217 TrpLysLeuLeuGlySerValValTrpAlaHisSerTrpGlnLeuLlePheArAlaTrp 236
Db 652 TGGAAAGCTGCTGGGCTCTGTGTCATAGCCCAACGCAAGAGCTGTGCTACTGCTGTAC 711

QY 237 lLeGlyPheLeuValLeuLlePheSerSerThrArGArGlyTrp 256

Oy	117	IsThrIySerLeuAlaSerSerCysLeuLeuIleLeuGIuIubheValMetIleValIaPhe	136
Db	527	TATGAGAAAGAGCTCGGAGGGGGCCCTTACATCTCGGAATTCGACTATCGTGGTCTTT	586
Oy	137	GIyLeuIdubheIleIleatGiletTrpSerAlaGIyScyScsAargyrraGgIyTrp	156
Db	587	GGCGTGGAGTACTTCGTCGGCATCTGGGCGGACGCTGCTGCGCGGACCGTGGC	646
Oy	157	GIuGIyArGIyLeuArGpheaIaArGlySProPheCysValIleAspThrIleValIle	176
Db	647	AGGGGGCGGCTCAGATTGTGGCCGAAACCGTTGTGTGATTACATCATGAGTCTCATC	706
Oy	177	AlaSerIleAlaValIaSerAlaIySthGIuGIyAsnIlePheaIaThrSerAlaLeu	196
Db	707	GCCTCATTCGGGTGCTGGCCGGCTCCGAGCGGACAGCTCTTCCATCTGGCGTTC	766
Oy	197	ArgSerLeuArGpPheLeuGIuIleLeuArGmetValArgMetAspArgrrgIyGlyThr	216
Db	767	CGAGAGCTCGGCTCTCTCGAGATTCTGGGATGATCCGATGGACCGGGGGAGGACAC	826
Oy	217	TrpIySLeuLeuGIySerValIaIyrraIaHisSerIySgluLeuIleIaIaTrpIy	236
Db	827	TGGAACTGCTGGGCTGTGTGTGTCATGCCCCACAGACAAGACGTGGTACTGCTGCTGAC	886
Oy	237	IleGIyPheLeuValLeuIlePheSerPheLeuValTyrLeuValGIuIyAspAla	256
Db	887	ATCGGCTTCCTTGTCTATCTATCTGGCGCTGCTTCGTGTACTTGGACAAGGGCGAG	946
Oy	257	AsnIySgluPheSerThrTyrAlaAspAlaLeuTyrIyGlyThrIleThrLeuThrThr	276
Db	947	AACGACCACTTGTACACCTACGCGGATGACACTGTGGGGCGTATCAGCGTGAACAC	1006
Oy	277	IleGIyTyrGIyAspIySthProLeuThrTrpLeuGIyArGleuLeuSerAlaIyPhe	296
Db	1007	ATTGGCTACGGGGACAAATACCCCCAGACCTGGAAAGGACAGCTCTTGGCGAACCTTC	1066
Oy	297	AlaLeuGIyIleSerPhePheAlaLeuProIaGIyIleLeuGIySerGIyPheAla	316
Db	1067	ACCCTCATCGGTGCTCTCTTCTTGGCGCTGGCTGAGGCACTTGGGGTCTGGGTTTCC	1126
Oy	317	LeuIySValGIuGIuGIuIaHisArgGIuIySthPheGIuIySArGAsnProAlaIa	336
Db	1127	CTGAAGGTTACGGAGCAGCACAGGCAAGACACTTGGAAAGGCGGAAACCCGGACACA	1186
Oy	337	AsnLeuIleGIuIySValIaTrpArgSerTyrAlaIaAsp	349
Db	1187	GGCTGTATCCAGTGGGCTGAGATTTCTACGCCACCAACTCTTGGCCACAGACTGACAC	1246
Oy	350	-----GIuIySerValSerIleAlaThrIyS-----	359
Db	1247	TCCACGTGGCAGTACTACGAGCAACGCTGACGTCCTGATCACTTGGCAAACTCA	1306
Oy	360	-----ProHisLeuIySAlaLeuHisThrCys-----	368
Db	1307	ACCTACGGGGCTCCAGACTTATCCCGCGCTGAACCACTGGAGCTGAGAAACTTC	1366
Oy	369	-----SerProIaAsn	372
Db	1367	AAGACTAAATCTGACTCGCTTACAGGAAGAGACCCCCCGGAGCGGCTTCCA--AGC	1423
Oy	373	GIuIySLeuSerPheIySgluArGValArgMetAlaSerProArgIyGIuIeIyS	392
Db	1424	CAGAAAGTCAATTGAAATATGCTGTC--TTCTCCAGCCCCGAGGCGTGGCTGCCAMG	1480
Oy	393	SerArgIaIaSerValIyIyS-----ArgArgSerProSerThrAspIleThrAla	410
Db	1481	GGGAAGGGGTCCCCGAGGCCACAGACTGTGAAGCGGCTCAACCCAGCCCAAGACAGCTTC	1540
Oy	411	GIuGIySerProThrIySValGIuIySserTrpSerPheAsnAspArgrraArgPheArg	430
Db	1541	GAGGACAGCCCGACAGAGGTGCCCAAGAACTGGAGCTTGGGAGCCGACGCGGGGACCC	1600
Oy	431	ProSerLeuArgLeuIySserSerGIuIySProValIleAspAlaAspThrAlaLeu	450

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Db 1601 CAGGCTTCCGATCAAGGGGCGCCGCTCACGGAGACACTCAGAA---GAAGCAAGCCTC 1657
QY 451 GLTThraspsvalyThraspGluLySGlncysaspValserValGluaspLeu 470
Db 1658 CCGGAGAGGAGACTTGGATGACAAAGAGCTGCCCTCAGAGTTTGGACCGAGACTG 1717
QY 471 ThrProLeuLeuThrasValleArgAlaIleArgIleMetLysPheHisValAlaLys 490
Db 1718 ACCCGGGGCTCAAGTACATCAGACATCAGACCGGTGTGTCTCATGGCTTCGTTCCAG 1777
QY 491 ArgLysPheLysGluThrLeuArgProTyrrAspValLysaspValIleGluGlnTyrrSer 510
Db 1778 CGGAAGTTCAGAGAGAGAGCTGCGGCTACGACCTGATGACGTCATCGACGACTCTCA 1837
QY 511 AlaGlyHisLeuaspMetLeuLysArgIleLysSerLeuGlnThrArgValAspGlnIle 530
Db 1838 GCGGCGCACCCTGACATGCTGCTCCGAAATTAAGAGCTTCAGTCCAGAGTGCACAGATC 1897
QY 531 LeuGlyLysGlyGlnIleThrSerAspLysLysSerArgGluLysIleThrAlaGlnHis 550
Db 1898 GTGGGGCGGGGCGCCACCATCAAGGAC---AAGGACCCGACCAAGGGCCCGCGGAGGCG 1954
QY 551 GluThrThraspLeuSerMetLeuGlyArgValValLysValGluLysGlnValGln 570
Db 1955 GAGCTGCCCGGAGAGACCCCGCATGATGGAGCGCTCGGAGAGTGGAGAAGAGTCTTG 2014
QY 571 SerIleGluSerLysLeuaspLysPcysLeuLeuaspIleTyrlngInValLeuArgLysGly 590
Db 2015 TCCATGAGAGAAAGACTGTGCTTCTGTTGAATATCTACATGCAG-----CGATGGGC 2068
QY 591 SerAlaSerAlaLeuAlaLeuAlaSerPheGlnIleProProPheGluCys-----607
Db 2069 -----ATCCCCCGACAGAGAGCCGAGGCTTAC 2095
QY 608 -----GluGlnThrSerAspTyrrGlnSerProValAspSerLysasp 621
Db 2096 TTTGGGGCCAAAGAGCCGGAAGCGCGGCCGCTACACAGCCGAGAGCCGAGCGGAG 2155
QY 622 LeuSerGlySerAlaGlnAsnSerGlyLysSerArgSerThrSerAlaAsnIleSer 641
Db 2156 -----CATGTCGACAGCAGCGCTGCATTTGTCAAGATGTCGCTCCAGCAGCTCC 2206
QY 642 ArgGlyLeuGlnPheIleLeuThrProAsnGluPheSerAlaGlnThrPheTyralLeu 661
Db 2207 ACGGGC-----2212
QY 662 SerProThrMetHisSerGlnAlaThrGlnValProIleSerGlnSerAspLysAla 681
Db 2212 -----2212
QY 682 ValAlaAlaThrasnThrIleAlaAsnGlnIleAsnThralaProLysProAlaAlaPro 701
Db 2213 -----CAGAAAGAACTTCTCGGGCGCCCGCGCGCGCC 2245
QY 702 ThrThrLeuGlnIleProPro-----ProLeuProAla 712
Db 2246 ---CCTGTCCAGTGTCCGCGCTCCACTCTCTGGCAGCCACAGACCCGCG-CCAGGG 2301
QY 713 IleLysHisLeuProArg-----ProGluThr-----LeuHis-ProAsnProAlaGln 728
Db 2302 CCAGGGGACCTCCCGCTGGGGGACGACGGCTCCCTGTGCGCATCCCGCGCGCTGC 2361
QY 728 yLeuGlnGluSerIleSerAspValThrThrCysLeuValAlaSerLysGluAsnValGln 748
Db 2362 CCACGAGCGGTCTGCTGCTGCTACGCGCGGGGCAACCGCGCATGGAGTCTCTGCG 2421
QY 748 nValAlaGlnSerAsnLeuThrLys-----AspArgSerMetArgLysSerPheasphe 766
Db 2422 GCAGGAGGAGACCCCGGCGTCCAGGCGCCCGGAGGGAGGAGGAGGAGGAGGAGGAGG 2473
QY 766 tGlyGlyGluThrLeuLeuSerValCysProMetValProLysAspLeuGlyLysSerLe 786

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Db 2474 -----GACACGTCCATCTCCATCCCGTGGAGCCAGGAGAGCTGGAGCTTCTT 2526
QY 786 uSerValGlnAsnLeuIleArgSerThrGluGlnLeuAsn 799
Db 2527 CAGGCGCTTCAGCATCTCCAGTCCAGAGGAGAGAGGAGGAGGAGGAGGAGGAGG 2566

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Search completed: January 11, 2003, 18:07:01
 Job time : 374 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - nucleic search, using frame_plus.p2n model

Run on: January 11, 2003, 17:57:22 : Search time 1959 Seconds
(without alignments)
7341.293 Million cell updates/sec

Title: US-09-810-796-5

Perfect score: 4547
Sequence: 1 MKDVSGRGRLVLSAARG.....STCKAGESTDALSLPHYKTK 888

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Command line parameters:

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-O=/cgn2.1/USPTO.spool/US09810796/funat.10012003_085456_22818/app_query.fasta.1.1031
-DB=EST -OPMT=fastcap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -STRAP=1 -END=1 -MATRIX=blousum62 -TRANS=human40.cdi -LIST=45
-DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09810796_ECGN_1_1191_etunac.10012003_085456_22818 -MCPU=6 -ICPU=3
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-WARN.TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_estl:*
10: gb_estl2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vit:*
22: em_gss_mam:*
23: em_gss_fun:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1258.5	27.7	997	10	BB609854
2	1099	24.2	658	10	BE158938
3	1043.5	22.9	679	10	BE647997
4	1024.5	22.5	632	10	BE624101
5	989	21.8	584	10	AW049888
6	925	20.3	734	12	BM532543
7	907.5	20.0	570	13	BI033850
8	902	19.8	547	13	BI034993
9	892	19.6	914	12	BF312386
10	864	19.0	908	12	BF240146
11	854.5	18.8	920	12	BF317072
12	835.5	18.4	1004	9	AT589812
13	834	18.3	1004	14	BO219245
14	831	18.3	506	12	BF959996
15	813	17.9	597	10	BE260338
16	802.5	17.6	625	10	BB666833
17	797	17.5	469	10	BE103175
18	792	17.4	491	12	BF959488
19	748	16.5	541	9	AT968605
20	729.5	16.0	771	9	AT517016
21	721	15.9	626	10	BB635544
22	719.5	15.8	528	12	BG732557
23	713	15.7	434	13	BI290441
24	700	15.4	477	17	AZ443500
25	697.5	15.3	698	13	BM640404
26	695	15.3	435	12	BF943257
27	689	15.2	502	9	AT182222
28	687.5	15.1	517	12	BF954375
29	664	14.6	568	14	BO339931
30	656.5	14.4	655	12	BF432555
31	651	14.3	469	9	AT864554
32	618.5	13.6	600	9	AU141948
33	618	13.6	448	14	BO285922
34	617.5	13.6	448	14	AV838434
35	603	13.3	427	12	BF523361
36	586.5	12.9	1082	17	CNS041K3
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40	559	12.3	537	12	BE703020
41	556	12.2	622	10	BE257127
42	541.5	11.9	567	13	BM253726
43	538.5	11.8	846	13	BI818397
44	535	11.8	671	10	BB617583
45	534.5	11.8	535	12	BF798694

ALIGNMENTS

RESULT 1
BB609854 997 bp mRNA linear EST 31-AUG-2001
LOCUS BB609854 RIKEN full-length enriched, adult male lung Mus musculus
DEFINITION CDNA clone 1200002P22 5', mRNA sequence.

ACCESSION BB609854
VERSION BB609854.1 GI:15390457
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. I (bases 1 to 997) Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J., Konno, H., Kouda

ACCESSION BE158938
 VERSION BE158938.1 GI:8621659
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 638)
 Dias Neto, E., Garcia Correa, R., Verjowski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H., Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.V.
 Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 20202663
 TITLE Contact: Simpson A.J.G.
 JOURNAL Laboratory of Cancer Genetics
 MEDLINE Ludwig Institute for Cancer Research
 COMMENT Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
 (<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=6t2-MRO-HM0404-210>)
 200-001-c046t3-2000-02-216t4-1)
 Seq primer: puc 18 forward
 High quality sequence stop: 657.
 location/Qualifiers
 1. 658
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="HT0404"
 /dev_stage="Adult"
 /note="Organ: head,neck; Vector: puc18; Site_1: Sma1; Site_2: Sma1; A mini-library was made by cloning products derived from ORSTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
 BASE COUNT 181 a 175 c 153 g 149 t
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 Alignment Scores:
 Pred. No.: 8,58e-105 Length: 658
 Score: 1099.00 Matches: 211
 Percent Similarity: 99.53% Conservative: 1
 Best Local Similarity: 99.06% Mismatches: 0
 Query Match: 24.17% Indels: 0
 Gaps: 0
 DB: 10
 US-09-810-796-5 (1-888) x BE158938 (1-658)
 QY 278 GlyTyrGlyAspLysThrProLeuThrTrpLeuGlyArgLeuLeuSerAlaGlyPheAla 297
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 Db 18 GGCTATGGAGCAAAACCTCCCTTAACCTGGCGGAGAGATTGCTTCTTCACAGCCTTGCA 77
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 QY 298 LeuLeuGlyIleSerPhePheAlaLeuProAlaGlyIleLeuGlySerGlyPheAlaLeu 317
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 QY 338 LeuIleGlnGlyValTrpArgSerTrpAlaAlaAspGlyLysSerValSerIleAlaThr 357
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QY 358 TrpLysProHisLeuLysAlaLeuHisThrCysSerProThrAsnGlnLysLeuSerPhe 377
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 DEFINITION UI-M-BH1-anr-g-09-0-UI 5', mRNA sequence.
 ACCESSION BE647997
 VERSION BE647997.1 GI:9973817
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 679)
 Bonaldo, M.F., Lennon, G. and Soares, M.B.
 Normalization and subtraction: two approaches to facilitate gene discovery
 Genome Res. 6 (9), 791-806 (1996)
 JOURNAL 97044477
 MEDLINE
 COMMENT Contact: Chin, H
 National Institute of Mental Health
 6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
 20892-9643, USA
 Tel: 301 443 1706
 Fax: 301 443 9890
 Email: mbest@nmi.nih.gov
 cDNA Library Preparation: M.B. Soares Lab Clone distribution:
 Researchers may obtain BMAP cDNA clones from RESEARCH GENETICS. It
 should be noted that Bento Soares is generating a small number of
 additional specialized non-redundant arrays of BMAP cDNAs whose
 availability will be considered under appropriate and limited
 collaborative arrangements
 Seq primer: M13 Reverse.
 location/Qualifiers
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 /note="Vector: pT73D-Pac (Pharmacia) with a modified
 polylinker. Site 1: Not I; Site 2: Eco RI; The
 NIH_BMAP_M.S2 library is a subtracted library derived from

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Db	123	AAGCGCTCTCTACACAGCAGCCAGAGCTCTCGCGCAACGTACAGTCGGGGTG	182
QY	77	GlnAsnTyrLeuTyrAsnValLeuGlnArgProArgLysTrpAlaPheLeuTyrHisAla	96
Db	183	CAGACCTATCTGTACACAGTGTGGAGGAGCCCGCGGTGGCGCTTCCTACACGGG	242
QY	97	PheValPheLeuLeuValPheGlyCysLeuIleLeuSerValPheSerThrIleProGlu	116
Db	243	TTTCGTTTTCTCTGTGTGGTGTGATTTGTCTGCTTTTCATCCATCCCTGAG	302
QY	117	HisThrLysLeuAlaSerSerCysLeuLeuIleLeuGluPheValMetIleValAlaPhe	136
Db	303	CATACAAATTTGGCTTCAAGTGCCTCTTAATTCCTGGACTTGTGATGATCTTGTCTT	362
QY	137	GlyLeuGluPheIleIleArgIleTrpSerAlaGlyCysCysArgTyrArgGlyTrp	156
Db	363	GGCTTGCAGTTCATCTTCAGATCTGTGCTCCAGGTGCTGTTCGTATAGAGATGG	422
QY	157	GlnGlyArgLeuArgPheAlaArgLysProPheCysValIleAspThrIleValLeuIle	176
Db	423	CNAGGAAACACGTGGTTGCTGAAACCATTTCTGTATATAGATACCATTTTCTCAGC	482
QY	177	AlaSerIleAlaValAlaSerAlaLysThrGlnGlyAsnIlePheAlaThrSerAlaLeu	196
Db	483	GCTTCATATAGCAGTTGTCTCTGCANAAACCTCAGGGTATATTTTGGCCACGTCACGGCTC	542
QY	197	ArgSerLeuArgPheLeuGlnIleLeuArgMetValArgMet	210
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RESULT	6
BG532543	
Locus	
Definition	BG532543 734 bp mRNA linear EST_03-APR-2001 60256210391 NIH_MGC_61 Homo sapiens CDNA clone IMAGE:4699776 5' , mRNA sequencing .
Accession	BG532543
Version	BG532543.1 GI:13524082
Keywords	EST.
Source	human. Homo sapiens
Organism	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 734)
Reference	NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
Authors	Contact: Robert Strausberg, Ph.D. Email: cgabbs@email.nih.gov
Journal	Tissue Procurement: ATCC
Comment	CDNA Library Preparation: CLONETECH Laboratories, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Data distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLCM1532 row: f column: 01 High quality sequence start: 699.

FEATURES
source

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/clone="IMAGE:469776"
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/tissue_type="embryonal carcinoma"
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/notes="organ: testis; Vector: pDNR-LIB (Clontech); Site_1: SfiI (ggcgccctcgccg); Site_2: SfiI (ggccatcatggcc); Double-stranded cDNA was prepared from cell line RNA. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGCGATTGAGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCGCGAGCGCCGATCAGT-dT(30)BN-3'

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(where B = A, C, or G and N = A, C, G, or T). Average insert size 1.75 kb (range 0.9-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH-MCC Library."

BASE COUNT	213 a	177 c	165 g	179 t
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Alignment Scores:				
Pred. No.:	2,05e-86	Length:	734	
Score:	925.00	Matches:	182	
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Query Match:	20.34%	Indels:	0	
DB:	12	Gaps:	0	

US-09-810-796-5 (1-888) x BG532543 (1-734)

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 Db 3 CAGATCCCACTCCTCTCCCAAGCATCAAGCATTCGCCAGGCCAAGAATCTGCACCT 62

QY 725 AsnProIaGlyLeuGlnGluSerIleSerAspValThrThrCysLeuValAlaSerLys 744

Db 63 AACCTGCAGGCTTACAGGAAGCATTTCTGACGTCACCACCTGCCCTTGTGCTCCAAG 122

QY 745 GlnAsnValGlnValAlaGlnSerAsnLeuThrLysAspArgSerMetArgLysSerPhe 764

Db 123 GAAATGTTCAAGTTGCACAGTCAAACTCACCACAAGGACCCTTCTATGAGGAAACCTTT 182

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[illegible]

865 AroSerSerG]nSer]eCvslvSA]ag]wg]uSerThrAsnA]alauSerLeuProHis 884

Dp 483 CGATCATCTCAGAGCATTTGTAAGGCAGGAGAACTACAGATGCCCCAGCTTGCTTCAT 542

QY 885 Vallysleulys 888

Db 543 GTCAAACTGAA 554

RESULT 7

LOCUS	BI033850	570 bp	mRNA	linear	EST 14-JUN
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ACCESSION BI033850

KEYWORDS. EST.

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Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

AUTHORS Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones,
Necajik, M. A., de Cidreira, W. T., Franco, V. A., Bandeira, C., Costa, P. D.

DB: 13 Gaps: 0

US-09-810-796-5 (1-888) x BI034993 (1-547)

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 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 REFERENCE 1 (bases 1 to 914)
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/
 TITLE Unpublished (1999)
 JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgaabs-r@mail.nih.gov
 Tissue Procurement: ATCC
 CDNA Library Preparation: Ling Hong/Rubin laboratory
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at: image.lnl.gov
 Plate: L1CM1020 row: d column: 07
 High quality sequence stop: 630.
 Location/Qualifiers
 1. 914
 /organism="Homo sapiens"

/db xref="taxon:9606"
 /clone="IMAGE:4127958"
 /clone_lib="NIH_MGC_19"
 /tissue_type="neuroblastoma"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: brain; Vector: pORF7; Site_1: XhoI; Site_2:
 EcoRI; cDNA made by oligo-dT priming. Directionally
 cloned into EcoRI/XhoI sites using the following 5'
 adaptor: GGCAAGGAG(G). Library constructed by Ling Hong
 in the laboratory of Gerald M. Rubin (University of
 California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies).
 Note: this is a NIH_MGC Library."

BASE COUNT 165 a 254 c 281 g 214 t

ORIGIN

Alignment Scores:
 Pred. No.: 8.58e-83 Length: 914
 Score: 892.00 Matches: 179
 Percent Similarity: 76.84% Conservative: 30
 Best local similarity: 65.81% Mismatches: 46
 Query Match: 19.62% Indels: 18
 DB: 12 Gaps: 4

US-09-810-796-5 (1-888) x BF312386 (1-914)

QY 78 AsnTyrLeuTyrAsnValLeuGluArgProArgGlyTyrAlaPheTLeTyrHisAlaPhe 97
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 DB 1 GATTTCCTCTACAAAGTGTGCTGAGCGCGCGCGCTGCGGCTTATCTACAGCGCTAC 60
 |||
 QY 98 ValPheLeuLeuValPheGlyCysLeuTLeuSerValPheSerThrTLeuProGluHis 117
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 DB 61 GTTTCCTCTGTTTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
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 QY 118 ThrLysLeuAlaSerSerCysLeuLeuTLeuGluPheValMetTLeuValPheGly 137
 |||
 DB 121 GAGAAAGGCTGAGGCGGCGCTCTACATCTCGAATCGTACTATGATGCTGTTTGGC 180
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 QY 138 LeuGluPheTLeuTLeuTLeuTLeuTLeuTLeuTLeuTLeuTLeuTLeuTLeuTLeuT 157
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 DB 181 GTGAGTACTCTGCGGATGCTGCGGATGCTGCGGATGCTGCGGATGCTGCGGATGCTG 240
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 QY 158 GlyArgLeuArgPheAlaArgLysProPheCysValTLeuAspThrTLeuValLeuTLeu 177
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 DB 241 GGGCGGCTCAAGTTGGCCCGGAAACCGTCTGTGATGATGATGATGATGATGATGATGAT 300
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 QY 178 SerTLeuAlaValSerAlaLysThrGlnGlnLysAlaPheAlaThrSerAlaLeuArg 197
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 DB 301 TCATTCGCGGTGCTGCGGATGCTGCGGATGCTGCGGATGCTGCGGATGCTGCGGATGCT 360
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 QY 198 SerLeuArgPheLeuGlnTLeuArgMetValArgMetAspArgGlyGlyThrTyr 217
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 DB 361 AGCGTGGCTTCCTGACAGATTCCTGCGGATGCTGCGGATGCTGCGGATGCTGCGGATGCT 420
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 QY 218 LysLeuLeuGlySerValValTyrAlaHisSerLysGluLeuTLeuTLeuTLeuTLeuT 237
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 DB 421 AAGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
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 QY 238 GlyPheLeuValLeuTLeuPheSerPheLeuValTyrLeuValGluLysAspAlaAsn 257
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 QY 258 LysGluPheSerThrTyrAlaAspAlaLeuTyrTyrGlyThrTLeuThrThrTLeu 277
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 DB 541 GACCAATTGACACCTACGCGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600
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 QY 278 GlyTyrGlyAspLysThrProLeuThrTyrPheGly-----ArgLeuLeuSer 293
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 DB 601 G--TACGGGGCAAGTACCCGACAGCTGGAAGCGCTTGGCGGAATTAACCTCA 658
 |||
 QY 294 AlaGlyPheAlaLeuLeuGlyTLeuSerPheAlaLeuProAlaGlyTLeuGlySer 313
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 DB 659 TCGGGT-----TCCTTTTCGCGTCTGCAAGGGGATCTGGGGGCT 700

Qy	314	gLYpHAlaLeuLyValcInglInGInHtAsrGgInLyHtSPheGInLytArGArGAsn	333
Db	701	GGGTTGGC----CCGTTAAGTCACAGAGCAGCGGACCTGGAGAGGGAAACCGG	757
Qy	334	ProAlaAlaAsnLeuLleGIncYsValTrpArGser	345
Db	758	AAGCGTTCA-----TCGGCGAGCT	775
RESULT 10			
LOCUS	BF240146	908 bp	mRNA
DEFINITION	601905649p1 NIH_MGC_54	Human sapiens	CDNA clone IMAGE:4133293 5',
ACCESSION	BF240146		mRNA sequence.
VERSION	BF240146.1	GI:11154069	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.		
TITLE	NIH-MGC http://mgc.nci.nih.gov/.		
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)		
COMMENT	Unpublished (1999)		
	Contact: Robert Strausberg, Ph.D.		
	Email: rstraub@mail.nih.gov		
	Tissue Procurement: ATCC		
	CDNA Library Preparation: CLONTECH Laboratories, Inc.		
	CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)		
	DNA Sequencing by: Incyte Genomics, Inc.		
	Clone distribution: MGC clone distribution information can be		
	found through the I.M.A.G.E. Consortium/LNL at:		
	http://image.lnl.gov		
	Plate: LICM1034 row: b column: 14		
	High quality sequence stop: 615.		
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	/db_xref="taxon:9606"		
	/clone="IMAGE:4133293"		
	/clone_lib="NIH-MGC_54"		
	/lssue_type="from chronic myelogenous leukemia"		
	/lab_host="DH10B (T1 phage-resistant)"		
	/note="Organ: bone marrow; Vector: pDNR-LIB (Clontech);		
	Site:1: StII (ggcgagctcgcc); Site:2: StII (ggcgatagcc		
); Double-stranded cDNA was prepared from cell line RNA.		
	5' and 3' adaptors were used in cloning as follows: 5'		
	adaptor sequence: 5'-CACGCCATTATGGCC-3' and 3' adaptor		
	sequence: 5'-ATTCTAGAGCGCAGCGCCACATG-AT(30)BN-3'		
	(where B = A, C, G, or T and N = A, C, G, or T). Average		
	insert size 1.75 kb (range 0.9-4.0 kb). 15/15 clones		
	contained inserts by PCR. This library was enriched for		
	full-length clones and was constructed by Clontech		
	Laboratories (Palo Alto, CA)."		
BASE COUNT	263 a	229 c	217 g
ORIGIN	199 t		
Alignment Scores:			
Pred. NO.:	7,49e-80	Length:	908
Score:	864.00	Matches:	205
Percent Similarity:	90.95%	Conservative:	6
Best Local Similarity:	88.36%	Mismatches:	11
Query Match:	19.00%	Indels:	12
DB:	12	Gaps:	0
US-09-810-796-5 (1-888) x BF240146 (1-908)			
Oy	667	SerGInaLthrGInValProLlSerGInSerAspGlySerAlaValAlaAlaThrAsn	686
Db	2	AGTCAGACACACAGCTGCCAATATGATCAAGCGATGCTCAGACATGGCAGCCACCAAC	61
Oy	687	ThrLleAlaAsnGInLleAsnThrAlaProLySerProAlaAlaProThrThrLleGInLle	706

Db	62	ACATTGGCAACCCTAAATAATAGCGCACCCAGCAGGCCCCAACCAACTTTACAGATC	121
QY	707	ProProPiePleuProAlaIlelyshIsleUpProAqPProglUthrLeuHisproaspRo	726
Db	122	CCACCTCCTCTCCACGCCATTCAGCATCTTGCCCGAGGA-GAAACTCTCACCTTAACCT	180
QY	727	AlaagLyLeugInguSerIlseerAspaValThrThrcySLeuValAlaSerLysLuasn	746
Db	181	GCAGGCTTACAGGAAGAAGCTTCTCAGCGCACACCTGCTGCTGTCCACAGGAAT	240
QY	747	ValGlInvalAlaGlnSerAsnLeuthrIlysAsparGserMetArgLysSerPheaspmet	766
Db	241	GTTTCAGGTTGACACGTCAAATCTCACCAAGGACCTTCTATCAGGAAAAGCTTTGACATG	300
QY	767	GIjgLyglUthrLeuLeuSerValCysPrometValProlYsAspLeuGIlySerLeu	786
Db	301	GGAGGGAANAACCTGTGTGCTCTCTGTCCCATAGGTGCCGAAGACTTGGCAATCTTTG	360
QY	787	SerValGlnAsnLeuIleArgSerThrgluLeuasnlleglInLeuSerGIlySerGIu	806
Db	361	TCTGTGC AAAACCTGATCAGGTGCGACCGACGAACTGATATACAACCTTTCAGGAGTCTG	420
QY	807	SerSerGIlySerArgGIlySerGIlnAspPheryrrPolySTTPArgILysSerLeu--P	826
Db	421	TCAAGGGCTCCAGAGGCAG-CMAGATTTTTAACCCCAATGAGGGAATCCAAAAATGGTT	479
QY	826	heIIeThrAspLeuIuValGIly--ProgluGIuThrgIuThrAsp--ThrpheAspAla	845
Db	480	TATATAAGTAGTAAGAGGTGGGTCCCGACAGAGACAGACAGACCACTTTGATGCGC	539
QY	845	IapProGlnProAlaArgGLuaAlaI-PheAlaserAspSerLeuarqThrgIylArgSer	864
Db	540	CACGAGCTGCCCGGGGAAAGCTGCTTTGATTACAGAACTCTAAAGACGTAAGGCTCA	599
QY	865	ArgSerSerGlnSerIle-CysLysAla-IjgLyglUser-TPhrAspAlaLeuSer-LeuPr	883
Db	600	CGATATATCTCAGACGATTTTGTAMGCCAGGAGACAGTTACAGATGCCCTTCAGGTGCC	659
QY	883	OhiSValLysLeuIys 888 :::	
Db	660	TCATGTCAAACTTGAA 675 :::	
RESULT 11			
LOCUS	BF317072	920 bp	mRNA linear EST 21-NOV-2000
DEFINITION	60190347OF1 NIH_MGC_19 Homo sapiens CDNA clone IMAGE:4136200 5',		
ACCESSION	BF317072		
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.		
TITLE	1 (bases 1 to 920)		
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)		
COMMENT	Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgaabs-r@mail.nih.gov Tissue Procurement: ATCC CDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov Plate: ILICM1041 row: K column: 17 High quality sequence stop: 714. Location/Qualifiers 1..920		
FEATURES			
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Db	2	GCGTGGGCGTTACATCAACAGCCCTACGTGTTCTCCTGGTTTTTCCTTGCCCTGTCGTCG	61
Qy	109	SerValPheSerThrIleProGluHisThrLysLeuAlaSerSerCysLeuLeuIleu	128
		: :	
Db	62	TCTGTGTTTCCACCATCAGAAGACTAGAAAGAGCGGAGGGGCCCTCTACATCTCG	121
Qy	129	GluPheValMetIleValAlaPheGlyLeuGlnPheIleIleArgIleTrpSerAlaGly	148
		:: :: : ::	
Db	122	GAATTCTGCATTCACGTCGTGTTGGGCGTGAGACTTCGTGGCGGACTGCGGATCGGCGCAGGC	181
Qy	149	CysCysCysArgTryrTrpGlyTrpGlnGlyArgLeuArpPheAlaArqLysProPheCys	168
		: : : : : : : : : : : : : :	
Db	182	TGCTGCTCCCGGTACCGTGGGTGAGGGGGGGCGCTCAAGTTGGCCGMAAACCTTCTGT	241
Qy	169	ValIleAspThrIleValIleuIleAlaSerIleAlaValAlaSerAlaLysThrGlnGly	188
		: : : : : : : : : : : : :	
Db	242	GTGATTCACATCACAGTGCTCATCGCCCTCCATTCGGGTGCGCCGCCGCGTCCAGGGC	301
Qy	189	AsnIlePheAlaThrSerAlaLeuArgSerLeuArpPheGlnIleLeuArgMetVal	208
		: : : : : : : : : : : : :	
Db	302	AACGCTTTGGCCACAATCGCGCTCCGAGCCTGGCGCTTCCTCGCAGATTCTGGGATGATC	361
Qy	209	ArgMetAspArgArGlyGlyThrTrpLysLeuGlnGlySerValValTyraAlaHisSer	228
		: : : : : : : : : : : : :	
Db	362	CGCATGACGCGCGGTGAGCACCCTGGAGCGTCGTGGCGCTGTGGTCTAAGCCACAGC	421
Qy	229	LysGluLeuIleThrAlaTrpTryrIleGlyPheLeuValLeuIlePheSerSerPheLeu	248
		: : : : : : : : : : : : :	
Db	422	AAGAGCGGGTGCACCTGGTGTACATCGGCTTCTTGTCTCATCTCGGCTCGTTCCTG	481
Qy	249	ValTyrrLeuValGluLysAspAlaAsnLysGluPheSerThrTyraAlaAspAlaLeuTrp	268
		: : : : : : : : : : : : :	
Db	482	GTGTACTTGGCAGAGAAAGAGAGACACCACTNTGACACTACCGCGAGTCACTGTGG	541
Qy	269	TrpGlyThrIleThrIleuThrThrIleGlyTyrrGlyAspLysThrProLeuThrTrpLeu	288
Db	542	TGGNCCCTGATCAGCTGACCACTTGGCTACNGTGCACAGTACCCCCAACCTTGCAA-	600
Qy	289	GlyArgLeuLeuSerAlaGlyPhe	296
		: : : : : : : : : : : : :	
Db	601	CGCAGGCTTTCGCMGTACCTTC	624
RESULT_13			
LOCUS	BQ219245	1004 bp mRNA linear EST 02-MAY-2002	
DEFINITION	AGENCOURT_7506202 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:6017909		
	5', mRNA sequence.		
ACCESSION	BQ219245		
VERSION	BQ219245.1	GI:20400645	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.		
REFERENCE	1 (bases 1 to 1004)		
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/-		
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)		
COMMENT	Unpublished (1999)		
	Contact: Robert Strausberg, Ph.D.		
	Email: csapsb@emall.nih.gov		
	Tissue Procurement: ATCC		
	cDNA Library Preparation: Life Technologies, Inc.		
	DNA Sequencing by: Agencourt Bioscience Corporation		
	Clone distribution: MGC Clone distribution/LINM information can be		
	found through the I.M.A.G.E. Consortium/LINM at:		
	http://image.lnl.gov		
	plate: L1AM13217 row: P column: 06		
	High quality sequence stop: 413.		
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	/db_xref="taxon:9606"		

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Db	3 GCAGGCTGCTGCTGCGCGGAGACCGTGGCTGGAGGAGGCGCGCTCAAGTTTGGCCGAAACCG	67.68%	Matches: 180	180
QY	167 PheCysValIleAspThrIleValIleuIleAlaSerTleAlaValSerAlaTysThr	60.61%	Conservative: 21	21
Db	63 TTCTGTGATTGACATCATGTGTCATGCTCCATTCGGTGGTGGCGCGCTCC	18.34%	Mismatches: 65	65
QY	187 GInglyAsnIlePheAlaThrSerAlaLeuArgSerLeuArgPheLeuGlnIleLeuArg		Indels: 31	31
Db	123 CAGGCAAGAGCTTGTCCCATCTGGCGCTCCGAGCGAGCTGGCTTCTCGAGATTTCGCG		Gaps: 5	5
QY	207 MetValArgMetAspArgArglyTThrTPlysLeuLeuGlySerValIValTyrAla			
Db	183 ATGATCCGATGAGCCGCGGCGGAGGAGCACCCTGGAACCTGTGGCGCTGTGGTATAGCC			
QY	227 HisSerIysGluLeuLeuThrAlaTTPyrIleGlyPheLeuValLeuIlePheSerSer			
Db	243 CACAGCAAGAGAGCTGGTCTACCTGCTGTACATTCGCTCTTGTGTCTCATCTCGCTCG			
QY	247 PheLeuValTyrLeuValGluIysAspAlaAsnIysGluPheSerThrTyrAlaAspAla			
Db	303 TTCCTGGTACTTGGCAGAGAGGAGGAGACACACACATTGTACACCTACCGCGATGCA			
QY	267 LeuTTPrgIlyThrIleThrLeuThrIleIleGlyTyrGlyAspIysThrProLeuThr			
Db	363 CTCTGTGGGCGCTGTATACAGCTGACCCACCATTTGGCTACGCGGACAGTACCCCGAGACC			
QY	287 TrpLeuGlyArgLeuLeuSerAlaGlyPheAlaLeuLeuGlyIleSerPhePheAlaLeu			
Db	423 TGGACGGGCAAGCTCTCTTGGCGCAACCTTACCTCTACGGGGCTCTCTTGGCTCTG			
QY	307 ProAlaGlyIleLeuGlySerGlyPheAlaLeuIysValGlnIleGlnIleAspArgIlys			
Db	483 CCGCAGGCACTTTGGGGCTGTGGTTTGCCTGTAAGGAGTAAAGCAGCAGCTGCGACAAG			
QY	327 His-PheGluIysArgArgAsnProAlaAlaAsnIleIleGlnIysValTTPraGserTyr			
Db	543 CACTCTTGAAGAAAGGCGGAGCCCGCA-----			
QY	346 AlaAlaAspGluIysSerValSerTleAlaIleThrTPlysProHisIleuIysAlaLeuHi			
Db	571 -----ACCAAGGCTGATGCCATTCGCGCTTGAAG-----			
QY	366 sThrCysSerProThrAsnIlyLeuSerPheIysGluArgValArgMetAlaSerPr			
Db	601 ----ATTCTACGCGCAACCAACT-----CTCCGCGGCAACAACCTGCGCACTCC			
QY	386 CArgGlyGlnSerIle-----LysSerArgGlnAlaSerValGlyAspArgAsySerPr			
Db	648 CAACGGTGGCACTACTACCCAAAGCGGAGCGGATCAGCGTGGCCCCCAATGGACAGG			

Oy	404	oserrThraspVAl1YrrAspGluLySGlYCysgIncYsaSpValserValGIuasPlenThr	471
Dp	708	GGAACCGCCGCCGGGGGAAACCCTGGCCAACCCCAACCGTGGATATCATT--	765
Oy	424	nAspatgThrArgPheArgProSerLeuArgIeulySsrSergInPro	440
Dp	766	-----TTTCATTGTGTCCCATTTGCCTCTTAAGAGCCCCCACT	807
RESULT 14			
LOCUS	BF959996/c	506 bp	mRNA linear EST 22-JAN-2001
DEFINITION	QV2.NN0045-051200-526-g09 NN0045 Homo sapiens cDNA, mRNA sequence.		
ACCESSION	BF959996		
VERSION	BF959996.1	GI:12372721	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 506)		
AUTHORS	Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Britones,M.R., Nagal,M.A., da Silva,W.Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H., Brunstein,A.P., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.U. and Simpson,A.J.U.		
TITLE	Shotgun sequencing of the human transcriptome with ORF expressed sequence tags		
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)		
MEDLINE	20202663		
COMMENT	Contact: Simpson A.J.G. Laboratory of Cancer Genetics Ludwig Institute for Cancer Research Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil Tel.: +55-11-2704922 Fax: +55-11-2707001 Email: asimpson@ludwig.org.br This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?LI-QV2&t2-QV2-NN0045- 051200-526-g09&t3=2000-12-05&t4=1) Seq primer: puc 18 forward High quality sequence stop: 506.		
FEATURES			
source	Location/Qualifiers 1..506 /organism="Homo sapiens" /db_xref="taxon:9606" /clone_lib="NN0045" /def_stage="Adult" /note="Organ: nervous normal; Vector: puc18; Site_1: Smal; Site_2: SmaI; A mini-library was made by cloning products derived from ORSTS PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."		
BASE COUNT	125 a 108 c 104 g 168 t	1 others	
ORIGIN			
Alignment Scores:			
Pred. NO.:	8.84e-77	Length:	506
Score:	831.00	Matches:	163
Percent Similarity:	100.00%	Conservative:	1
Best local Similarity:	99.39%	Mismatches:	0
Query Match:	18.28%	Indels:	0
Dp:	12	Gaps:	0
US-09-810-796-5 (1-888) x BF959996 (1-506)			
OY	452	ThraspaspVal1YrrAspGluLySGlYCysgIncYsaSpValserValGIuasPlenThr	471
Dp	505	ACTATATGATATGATATGAAAAAGAGATCCAGTGCTGATGATATACGTGGAGAGACTTACC	446

QY	472	ProProLeuLysThrValIleArgAlaIleArgIleMetLysPheHisValAlaLysGly	491
Db	445	CCACCACCTTAAACGTCTCATTGACGATTCACAGATTATGAAATTTTCATGTTCGAAAAACGG	386
QY	492	LysPheLysGluThrLeuArgProTyrAspValLysAspValIleGluInTyrSerAla	511
Db	385	AAGTTTAAAGGAAACATTTACGTCCATATGATGTAAAGATGTCATTGACAAATATTCCTGCT	326
QY	512	GlyHisLeuAspMetLeuGlySarArgIleLysSerLeuGlnThrArgValAspGlnIleLeu	531
Db	325	GGGTCACTGGACATGTTGTGTAGAAATTTAAAGCCTTCACAAACGCTGTTCATCAAAATTCCT	266
QY	532	GlyLysGlyGlnIlePheThrSerAspLysLysSerArgGlnLysIlePheArgLysHisGlu	551
Db	265	GGAAAAAGGCAATATCATTCAGATTAAGAAGACGCCGAGAAAAATAACACAGACATGAG	206
QY	552	ThrThrAspAspLeuSerMetLeuGlyArgValValLysValGluLysGlnValGlnSer	571
Db	205	ACCACAGACAGATCTCAGATTCCTCGGTCCGGTGCAGTCAAGTGTGAAAAACAGGTACAGTCC	146
QY	572	IleGluSerLysLeuAspCysLeuLeuAspIleTyrGlnGlnValLeuArgLysGlySer	591
Db	145	ATAGATATCAACACTGGACTGCTCTACTAGACATCTATCAACAGAGTCTTCGGAAAGGCTCT	86
QY	592	AlaSerAlaLeuAlaLeuAlaSerPheGlnIleProProPheGluCysGluInThrSer	611
Db	85	GGCTCAGCCCTCGCTTGGCTTCATTCAGATCCAGATCCACACTTTTGAATGTCAACAGACATCT	26
QY	612	AspTyrGlnSer	615
Db	25	GACTATCAAGCC	14
RESULT	15		
LOCUS	BE260338	597 bp	MRNA linear EST 26-OCT-2000
DEFINITION	601151405P1 NIH_MGC_19 Homo sapiens CDNA clone IMAGE:3507553 5',		
ACCESSION	BE260338		
VERSION	BE260338.1	GI:9131523	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.		
TITLE	1 (bases 1 to 597)		
JOURNAL	NIH-MGC http://mgc.nci.nih.gov/.		
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC)		
	Unpublished (1999)		
	Contact: Robert Strausberg, Ph.D.		
	Email: cgapbs-rt@mail.nih.gov		
	Tissue Procurement: ATCC		
	CDNA Library Preparation: Ling Hong/Rubin Laboratory		
	CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)		
	DNA Sequencing by: Incyte Genomics, Inc.		
	Clone distribution: MGC clone distribution information can be		
	found through the I.M.A.G.E. Consortium/LNLN at: image.lnl.gov		
	Plate: LNCM187 row: j column: 02		
	High quality sequence stop: 597.		
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	/note="Organ: brain; Vector: pOTB; Site_1: XhoI; Site_2:		
	EcoRI; CDNA made by oligo-dT priming. Directionally		
	cloned into EcoRI/XhoI sites using the following 5'		
	adaptor: GGCACGAG(G). Library constructed by Ling Hong		
	in the laboratory of Gerald M. Rubin (University of		
	California, Berkeley) using ZAP-CDNA synthesis kit		

GenCore version 5.1.3
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OM protein - nucleic search, using frame_plus.p2n model

Run on: January 11, 2003, 17:58:52 ; Search time 65 Seconds
(without alignments)
4189.676 Million cell updates/sec

Title: US-09-810-796-5
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
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Searched: 441362 seqs, 153338381 residues
Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
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and is derived by analysis of the total score distribution.

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ALIGNMENTS

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Sequence 95, Application US/09177650
Patent No. 6413719
GENERAL INFORMATION:
APPLICANT: Leppert, Mark F.
APPLICANT: Singh, Nanda
TITLE OF INVENTION: Charlier, Carole
TITLE OF INVENTION: KCMO2 AND KCMO3 - POTASSIUM CHANNEL GENES WHICH ARE
TITLE OF INVENTION: MUTATED IN BENIGN FAMILIAL NEONATAL CONVULSIONS (BFNC)
FILE REFERENCE: 2323-134
CURRENT APPLICATION NUMBER: US/09/177, 650
CURRENT FILING DATE: 1998-10-23
EARLIER APPLICATION NUMBER: 60/063,147
EARLIER FILING DATE: 1997-10-24
NUMBER OF SEQ ID NOS: 129
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 95
LENGTH: 3237
TYPE: DNA
ORGANISM: Homo sapiens
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NAME/KEY: CDS
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QY 665 Met1His1Ser1Gln1Ala1Thr1Gln1Val1Pro1le1Ser1Gln1Ser1Asp1Lys1Ser1Ala1Val1Ala1 684
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QY 685 Thr1Asn1Thr1le1Ala1sn1Gln1le1Asn1Thr1Ala1Pro1Lys1Pro1Ala1Ala1Pro1Thr1Leu 704
Db 2149 -----CAGAGAACTTCTCGGCGCGCCCGCGCGCGCC---CTGTCT 2187
QY 705 Gln1le1Pro1Pro----- 2187
Db 2188 CAGTGTCCGCTCCACCTCTCTGACAGCACAGAGCCAGCCCGC-CCAGGGCCACGGGCAC 2246
QY 716 Leu1Pro1Arg-----Pro1Gln1Thr-----Leu1His-Pro1Asn1Pro1Ala1Gly1Leu1Gln1 731
Db 2247 CTCCTCCGTGGGGACCAAGCGCTCCCTGTGTCGCATCCCGCGCGCTGCCACAGAGCG 2306
QY 731 user1le1Ser1Asp1Val1Thr1Thr1Cys1Leu1Val1Ala1Ser1Lys1Gln1Val1Gln1Val1Ala1 751
Db 2307 GTCCCTGTCCGCTTACAGCGGGGCAACCGCGCAGCATGAGATTCGTGCGGCGAGAGA 2366
QY 751 nSer1Asn1Leu1Thr1Lys-----Asp1Arg1Ser1Met1Arg1Lys1Ser1Phe1Asp1Met1Gly1Gly 769
Db 2367 CACCCCGGCTGACAGGCCCCCGAGGGAGGAGCCCTGCGGGAGACAC-----GA 2411
QY 769 uThr1Leu1eul1Ser1Val1Cys1Pro1Met1Val1Pro1Lys1Asp1le1Gly1Lys1Ser1Leu1Ser1Val1 789
Db 2412 CACGTCCATCTCCATCCGCTCGGTGACACAGAGAGAGTGTGAGCGTTCCTTACGGGCTT 2471
QY 789 nAsn1Leu1le1Arg1Ser1Thr1Gln1Gln1Leu1Asn 799
Db 2472 CAGCATCTCCAGTCCAGTCCAGAGAGAACCTTGAT 2502

RESULT 3
US-09-105-058C-22
Sequence 22, Application US/09105058C
Patent No. 6403360
GENERAL INFORMATION:
APPLICANT: Blamar, Michael A.
APPLICANT: Dworetzky, Steven
APPLICANT: Gribkoff, Valentin K.
APPLICANT: Levesque, Paul C.
APPLICANT: Little, Wayne A.
APPLICANT: Neubauer, Michael G.
APPLICANT: Yang, Wen-Pin
TITLE OF INVENTION: KONO POTASSIUM CHANNELS AND METHODS OF MODULATING SAME
FILE REFERENCE: 3053-4052
CURRENT FILING DATE: US/09/105,058C
CURRENT APPLICATION NUMBER: 1998-06-26
PRIOR FILING DATE: 1997-08-12
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 22
LENGTH: 2169
TYPE: DNA
ORGANISM: mouse
US-09-105-058C-22

Alignment Scores:
Pred. No.: 3,32e-166 Length: 2169
Score: 1790.50 Matches: 390
Percent Similarity: 65.16% Conservative: 72
Best Local Similarity: 55.01% Mismatches: 146
Query Match: 39.38% Indels: 101
DB: 4 Gaps: 18

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US-09-810-796-5 (1-888) x US-09-105-058C-22 (1-2169)

QY 17 AlaAlaArgGlyAspGlyLeuLeuLeuGlyThrArgAlaAlaThrLeuGlyGly 36
Db 100 TCCACAGCGAGCGCGGCTATCGCGGCTCCGAGCGCCCAAG-----CGC 150

QY 37 GAGGlyGlyLeuArgGlySerArgArgGlyLysGlnGlyAlaArgMetSerLeuGly 56
Db 151 GGCAGCGTTTGGACAGCGCGCGAGCGCGCGCGCGAGCC-----GGG 195

QY 57 LysProLeuSerThrThrSerSerGlnSerCysArgArgAsnValLysTyrArgArgVal 76
Db 196 AAGCCC-----CGGAAGCGCAAGCGCTTCTACCGCAAGCTG 231

QY 77 GlnAsnTyrLeuTyrAsnValLeuGlnArgProArgGlyTyrTrpAlaPheIleTyrHisAla 96
Db 232 CAGAAATTCCTTACAAACGCTAGAGCGCGCGCGCGCTGGCGTTTCATCTACACAGCC 291

QY 97 PheValPheLeuLeuValPheGlyCysLeuIleLeuSerValPheSerThrIleProGlu 116
Db 292 TACGTGTTCTTCTTACGTTCTCTCTGCTTGTCTTCTTGTGTTTCCACATCAGAG 351

QY 117 HisThrLysLeuAlaSerSerCysLeuLeuIleLeuGlnPheValMetIleValPhe 136
Db 352 TACGAGAGAGCTGTGAGGGGCGCTCTACATCTTGAATCGTACATGCGTATTC 411

QY 137 GlyLeuGlnPheIleIleArgGlyLeuTyrSerAlaGlyCysCysArgTyrArgGlyTyr 156
Db 412 GGTGTGAGTACTTGTGAGAGATGGGCTGCGAGCTGCTGCTGCTGCTGCTGCTGCTG 471

QY 157 GlnGlyArgLeuArgPheAlaArgLysProPheCysValIleAspThrIleValLeuIle 176
Db 472 AGGCGCAGCTCAAGTTGCCAGAGCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 531

QY 177 AlaSerIleAlaValValSerAlaLysThrGlnGlyAsnIlePheAlaThrSerAlaLeu 196
Db 532 GCCTCCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 591

QY 197 ArgSerLeuArgPheLeuGlnIleLeuArgMetValArgMetAspArgArgGlyTyr 216
Db 592 CGGAGCTTGGCTTGTGCAATCTTGGGATGATCCGATATGAGCGAGGGGTGGACCC 651

QY 217 TrpLysLeuLeuGlySerValValTyrAlaHisSerLysGlnLeuIleThrAlaTyrTyr 236
Db 652 TGGAGCTCTTGGATGGATGCTAGCTACGCTCAGAGCAGAGAGCTGCTGCTGCTGCTG 711

QY 237 IleGlyPheLeuValLeuIlePheSerSerPheLeuValTyrLeuValGlnLysAspAla 256
Db 712 ATTGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 771

QY 257 AsnLysLysLeuSerThrTyrAlaAspAlaLeuTyrTrpGlyThrIleThrIleThrThr 276
Db 772 AATGACCACTTGTGACCTTACGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 831

QY 277 IleGlyTyrGlyAspLysThrProLeuThrTrpLeuGlyArgLeuLeuSerAlaGlyPhe 296
Db 832 ATGGCTACAGCGGAGCAGTACCTCAGACCTGGAACGGAGGCTGCTGCTGCTGCTGCTG 891

QY 297 AlaLeuLeuGlyIleSerPhePheAlaLeuProAlaGlyIleLeuGlySerGlyPheAla 316
Db 892 ACCCTCATTTGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 951

QY 317 LeuLysValGlnGlnGlnHisArgGlnLysHisPheGlnLysArgArgAsnProAlaAla 336
Db 952 CTGAAATCCCAAGAGCAGATCGGCAAAACACTTTGAGAAACGGCGGAGACCTGCGGCA 1011

QY 337 AsnLeuIleGlnCysValTyrArgSerTyrAlaAlaAsp----- 349
Db 1012 GGTCTGATCCAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1071

QY 350 -----GlnLysSerValSerIleAlaThrTrpLys-----ProHis 361
Db 2041 CTTGCCAGTGTCTCTCCCTCACCTCG 2067

Db 1072 TCCACGTGCGAGTACTAGAGCGGAGCTCATCTGCCATGATAGACATCATCCACT 1131

QY 362 LeuLysAlaLeuHisThrCys----- 368
Db 1132 CTGAACCACTGTGAGCTGCTGAGGAATCTCAGAGCAAAATCTGACTCACCCTTACAGAG 1191

QY 369 -----SerProThrAsnGlnLysLeuSerPheLysGlnArgValArg 382
Db 1192 GAGCCACAGCAGAGCATCAGCA-----AGTCAGAGTCTGATGTAAGATGCTGCTGCTG 1245

QY 383 MetAlaSerProArgGlyGlnSerIleLysSerArgGlnAlaSerValGlyAsp----- 400
Db 1246 TTTCTCCAGCCCGCCAGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1305

QY 401 ArgArgSerProSerThrArgPheArgPheArgPheArgPheArgPheArgPheArgPhe 420
Db 1306 CGGCGGTCCCGCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1365

QY 421 TrpSerPheAsnAspArgThrArgPheArgPheArgPheArgPheArgPheArgPheArgPhe 440
Db 1366 TGGAGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1425

QY 441 LysProValIleAspAlaAspThrAlaLeuGlyThrAspAspValTyrAspGlnLysGly 460
Db 1426 CGGCAAGATTCAGAGAGCAAGCTCCCT---GGGAGGACATCTGAGAGGAGCAACAGAGC 1482

QY 461 CysGlnCysAspValSerValGlnAspLeuThrProProLeuLysThrValIleArgAla 480
Db 1483 TGTAACTGGAGGTTTGTGACTGAGATCTTACCTGCTGCTGCTGCTGCTGCTGCTGCTG 1542

QY 481 IleArgIleMetLysPheHisValAlaLysArgLysPheLysGlnLysLeuArgProTyr 500
Db 1543 GGTGTGTATGTGGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1602

QY 501 AspValLysAspValIleGlnGlnTyrSerAlaGlyHisLeuAspMetLeuCysArgIle 520
Db 1603 GATGTATGAGCAGCTCAGCAAGACTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1662

QY 521 LysSerLeuGlnThrArgValAspGlnIleLeuGlyLysGlnIleThrSerAspLys 540
Db 1663 AAGACCTGCAAGTCAGAGTGGACAGACATTTGSGGCGGGCCCAACATTAACGAT--- 1719

QY 541 LysSerArgGlnLysIleThrAlaGlnHisGlnThrThrAspAspLeuSerMetLeuGly 560
Db 1720 AAGGATCGCAGCAAGCGCCAGCGAAACGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1779

QY 561 ArgValValLysValGlnLysGlnValGlnSerIleGlnSerLysLeuAspCysLeuLeu 580
Db 1780 CGGCTTGGAGGTGGAGAAACAGTCTTGTCCATGTGAAGAAAGCTGCTGCTGCTGCTGCTG 1839

QY 581 AspIleTyrGlnValLeuArgLysGlySerAlaSerAlaLeuAlaLeuAlaSerPhe 600
Db 1840 AGCATCTATACACAG-----AGAAATGGC----- 1863

QY 601 GlnIleProPheGlyCys-----GlnGlnThrSer 611
Db 1864 ---ATCCACACAGAGAGAGAGAGCTATTTGGGCGCAAGAGACCTGAGCGCGCACCA 1920

QY 612 AspTyrGlnSerProValAspSerLysAspLeuSerGlySerAlaGlnAsnSerGlyCys 631
Db 1921 CCTTACCAAGCCCGAGAGAGCGGTGAC-----CATGCGAGCAACAGATGGCTGT 1971

QY 632 -----LeuSerArgSerThrSerAlaAsnIleSerArgGlyLeuGlnPheIleLeu 648
Db 1972 ATCATTAAGATCGTCCGCTCCACAGCTCT----- 2001

QY 649 ThrProAsnGlnPheSerAlaGlnThrPheTyrAlaLeuSerProThrMetHisSerGln 668
Db 2002 -----ACGGCGCAGAGAGAACTACGACAGCACCAGCAGCATC-----CCC 2040

QY 669 AlaThrGlnValProIleSerGlnSer 677
Db 2041 CTTGCCAGTGTCTCTCCCTCACCTCG 2067

Pred. No.: 7,43e-164 Length: 2273
 Score: 1767.00 Matches: 394
 Percent Similarity: 63.40% Conservative: 79
 Best Local Similarity: 52.82% Mismatches: 184
 Query Match: 38.86% Indels: 90
 DB: 4 Gaps: 17

US-09-810-796-5 (1-888) x US-09-177-650-88 (1-2273)

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OY 17 AlaAlaArgGlyAspGlyLeuLeuLeuLeuGlyThrArgAlaAlaThrLeuGlyGly 36
    ::::: ||| |||::: |||::: |||
Db 100 TCCACACCCGAGCGCNCNCTACTCATCGCGGCTCCGAGGCCGCCAAG-----CGC 150

OY 37 GlyGlyGlyLeuArgGlySerArgArgGlyGlyGlyGlyAlaArgMetSerLeuLeuGly 56
    ||| |||::: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 151 GGCANCNNTTGGAGCAAGCCGCGAGCGGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGG 195

OY 57 LysProLeuSerTyrThrSerSerGlnSerCysArgArgAsnValLysTyrArgArgVal 76
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 196 AAGCCCCCNMAAN-----CGCACGCCCTTCTACCCCAAGCTG 231

OY 77 GlnAsnTyrLeuTyrAsnValLeuGluArgProArgGlyTyrAlaPheIleTyrHisAla 96
    ||| |||::: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 232 CAGAAATTCCTACACAGCTGCTAGAGCGGCCCGCGGCTGCGGCTTCACTACACAGCGCC 291

OY 97 PheValPheLeuLeuValPheGlyCysLeuIleLeuSerValPheSerThrIleProGlu 116
    ::::: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 292 TACGTTCTCTCTGCTGCTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 351

OY 117 HisThrIysLeuAlaSerSerCysLeuLeuIleLeuGluPheValMetIleValAlaPhe 136
    ::::: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 352 TACGAGAGAGCTCTGAGAGGCGCCCTTACATCTTGAAGAAAGTGATGCTATGCTGATATTC 411

OY 137 GlyLeuGluPheIleIleArgIleThrSerAlaGlyCysCysArgTyrArgIleTyr 156
    ||| |||::: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 412 GGTGTGTGACTTGTGTGAGATCTGGGCTGCGAGGCTGCTGTGCTGCTGCTGCTGCTGCTG 471

OY 157 GlnIlyArgLeuArgPheAlaArgIysProPheCysValIleAspThrIleValIleuile 176
    ::::: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 472 AGGGGAGGCGCTCAGATTGCCAGAGAGCGCTTCTGTGATGATGATGATGATGATGATGATG 531

OY 177 AlaSerIleAlaValSerAlaLysThrGlnIlyAsnIlePheAlaThrSerAlaLeu 196
    ||| |||::: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 532 GCCCCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 591

OY 197 ArgSerLeuArgPheLeuGlnIleLeuArgMetValArgMetAspArgArgIleGlyThr 216
    ||| |||::: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 592 CGGAGCTTGGGCTTGTGCAAAATCTTGGGATGATCCGATATGAGCCGAGGGGCTGGCACCC 651

OY 217 TrpIysLeuLeuGlySerValValTyrAlaHisSerIysGluLeuIleThrAlaTrpTyr 236
    ||| |||::: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 652 TGGAGGCTTGGGATGCTGATGCTACGCTACACACAGAGAGCTGTGATGCTGTGCTGTGATC 711

OY 237 IleGlyPheLeuValLeuIlePheSerSerPheLeuValTyrLeuValGluLysAspAla 256
    ||| |||::: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 712 ATTGGCTTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 771

OY 257 AsnIysGluPheSerThrTyrAlaAspAlaLeuTrpTrpGlyThrIleThrLeuThrTrp 276
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 772 AATGACACACTTGAACCTACGACAGATCAGCTGTGGGCTGTAGTACACCTGACGAGACC 831

OY 277 IleGlyTyrGlyAspLysThrProLeuThrTrpLeuGlyArgLeuLeuSerAlaGlyPhe 296
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 832 ATTTGGCTACGGGAGCAGTACCTCAGACCTGAGAGCGGAGGAGGCTGTGCGACGACCTTT 891

OY 297 AlaLeuLeuGlyIleSerPhePheAlaLeuProAlaGlyIleLeuGlySerGlyPheAla 316
    ||| |||::: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 892 ACCCTCATTTGTTGTTGCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 951

OY 317 LeuIysValGlnGlnGlnHisArgGlnLysHisPheGluLysArgArgAsnProAlaAla 336
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 952 CTGAAATCCAGAGCAGCATGGCAAAAACACTTTGAGAAACGGCGGAGAACCTCGCGGCA 1011
  
```

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OY 337 AsnLeuIleGlnCysValTrpArgSerTyrAlaAlaAsp----- 349
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1012 GGTGTGATCCAGTCTGCTGCTGAGATTTCTATGCTACTAACCTCTCAGCAGCAGCTGCGAC 1071

OY 350 -----GluLysSerValSerIleAlaThrTrpIlyProHisLeuLys 363
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1072 TTCACGTGGCAGTACTACGACGAGNACATGCTGTCCTCATGTATACGCTACACAACTCA 1131

OY 364 -----AlaLeuHisThrCysSerProThrAsnGln----- 373
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1132 ACCTATGGGCGCTCAGACATCATCCACTCTGAGACAGAGCTGAGCTGTGTGAGATTC 1191

OY 374 -----LysLeuSerPheLysGluArgValArg-----MetAlaSerPro 386
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1192 AAGACAAATCTGAGCTCACTCACTTCAAGAGAGAGCAGACAGCCATCACCAGAGCCCC 1251

OY 387 ArgGlyGlnSerIleLysSerArgGlnAlaSerValGlyAsp-----ArgArgSerPro 404
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1252 CGAGGATGGCTGCGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1311

OY 405 SerThrAspIleThrAlaGluGlySerProThrIysValGlnLysSerTrpSerPheAsn 424
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1312 AGTCGGATCAGAGTCTTGTATGACAGCCCGAGCAAGGTGCCAAGAGCTGGAGCTTTGGT 1371

OY 425 AspArgThrArgPheArgProSerLeuArgLeuLysSerSerGlnProLysProValIle 444
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1372 GACCGCAGCGCAGCAGCGCAGGCTTCCGATCAAGAGGCTGCTGATCCCGGAGCAATTCA 1431

OY 445 AspaIasPThrAlaLeuGlyThrAspAspValTyrAspGluLysGlyCysGlnLysAsp 464
    ::::: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1432 GAACAACAGAGCCCTCCCGGGGAGGAGACATCTAGAGGACACACAGAGCTGTACTGCGAG 1491

OY 465 ValSerValGluAspLeuThrProProLeuLysThrValIleArgAlaIleArgIleMet 484
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1492 TTGTGTGACTGAGATCTTACCCCTGCGCTCAAACTYACACAGAGCGCTGTGTATG 1551

OY 485 LysPheHisValAlaLysArgLysPheLysGluThrLeuArgProTyrAspValLysAsp 504
    ::::: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1552 CGGTTCTTGTGATCTTAAGCGAAGATTCAGAGAGTGTGCGCCCATGATGTGTGTGAGAC 1611

OY 505 ValIleGluGlnTyrSerAlaGlyHisLeuAspMetLeuCysArgIleLysSerLeuGln 524
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1612 GTCATCAACAGTACTCGGCTGGAGACTGTGATATGTGTCCTGATCAAGAGCTGTGAG 1671

OY 525 ThrArgValAspGlnIleLeuGlyLysGlyGlnIleThrSerAspLysLysSerArgGlu 544
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1672 ACCAGATGGACAGATTTGGGCGGCGGCCCAACAATAAACGAT---AAGATTCGCACC 1728

OY 545 LysIleThrAlaGluHisGluThrThrAspAspLeuSerMetLeuGlyArgValValLys 564
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1729 AAGAGCCGACGGAGAACGAGCTGCCGAGAGCCCAACATGATGAGCGGCTTGGGAGAG 1788

OY 565 ValGluLysGlnValGlnSerIleGlnSerLysLeuAspCysLeuLeuAspIleTyrGln 584
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1789 GTGAGAAACAGGCTTGTCTCATGAGAAAGAGCTCGACTTCTTGTAAGATCATATCA 1848

OY 585 GlnValLeuArgIysGlySerAlaSerAlaLeuAlaLeuAlaSerPheGlnIleProPro 604
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1849 CAG-----AGAAATGGGATCCAAACAGACAGAGAGGCGCTTTTGGGGCCCAAG--- 1899

OY 605 PheGluCysGluGlnThrThrSerAspTyrGlnSerProValAspSerLysAspLeuSerGly 624
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1900 ---GAGCCTTAGCCGGGAGCACCTTACACAGCCCAAGAGGACAGCCCGGAGC----- 1947

OY 625 SerAlaGlnAsnSerGlyCys-----LeuSerArgSerThrSerAlaAsnIleSer 641
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1948 CATGCAAGACAGATGCTGTATCATTAAGATGTGTCGCTCCAGCTCAGCTACAGG---GCC 2005

OY 642 ArgGly-----LeuGlnPheIleLeuThrProAsnGlu 652
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2006 AGAGGAAGTACAGCAGACCCCGACCATCCCTGCGCAGTGTCTCCCTCCACCTCTGCT 2065

OY 653 PheSerAlaGlnThr-----PheTyr 659
  
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OY	457	AspGluIuYsgLyScLyngCysAspValSerValGluAspLeuThrProProLeuIuYsThr	476
Db	1438	GAAGACAGGGGGCTATGTGGAAATGACTTCCCATCCAGACATGATGCCACCTTCAAGGCC	1497
OY	477	ValIleArgAlaIleArgIleMetCysPheHisValAlaIuYsArgIuYsPheIuYsGluThr	496
Db	1498	GCATTCGGAGCGCCACAGATTTCTACATTCGCGTCTCTATATAAAAAATTTAAAGAGACT	1557
OY	497	LeuArgProIuYsAspValIuYsAspValIleGluIuYsSerAlaGluHisIleAspMet	516
Db	1558	TTGAGGCCCTTACAGTGTGAAGAGATGATATTGACGATATTCTGCCGGCATCTGCACATG	1617
OY	517	LeuCysArgIleIuYsSerLeuGluThrArgValAspGluIleIuYsGlyGluIle	536
Db	1618	CTTCCAGGATTAAGTACCTTTCAGACAGATATGATTTTCACCCCTCGACCTGCC	1677
OY	537	ThrSerAspIuYsSerArg	543
Db	1678	TCCACGCCCAAAACACAGAAGATCTCAGAAAGGTCAGACATTCACCTCCATCCACGAA	1737
OY	544	-----GluYsIleThrAlaGluHisIuThr-----AspAspLeuSer	557
Db	1738	TCGCCAGGATGATACCATTTGTAGCCAGACCATCCATCAGAAATCGAAGCAAAAGC	1797
OY	558	MetLeuGlyArgValValIuYsValGluIuYsGluValGlnSerIleGluSerIuYsAsp	577
Db	1798	ATGATGGGGAAGTTTGTAAAGTTGAAAGACAGGTTCCAGACATGGGGAAGAGCTGCAC	1857
OY	578	CysLeuAspIleIuYsArgGluIuYsValLeuArg	588
Db	1858	TTCCCTGTGGATTTGCACATGCACACATGAAAGCGTTGCAGTGCAGTCCAGGAGTAT	1917
OY	589	-----LysGlySerAlaSerAlaLeuAlaLeuAlaSerPheGluIleProIuPhe	605
Db	1918	TACCCACCAAGGAGGCACCTCTCTG-----CCAGCT	1947
OY	606	GluCysGluGlnThrSerAspIuYsGlnSerProValAspSerIuYsAspLeuSerGlySer	625
Db	1948	GAGCAGAGAAGAAGAGAGCAACAGGTATTC--GATTGTGAACCATCATCTGCAAC	2004
OY	626	AlaGluAsnSerIuYsCysLeuSerArgSerThrSerValAsnIleSerArgGlyLeuGln	645
Db	2005	TATTTCGAGACAGGCCCGCCGAGACACCCCTACAGCTTCAC-----	2046
OY	646	PheIleLeuThrProAsnGluPheSerAlaGluThrPheTyAlaLeuSerProIuMet	665
Db	2047	---CAAGTCACATTGACAAAGCACCCCTATGGCTTTTTCACATGACCT-----	2097
OY	666	HisSerGlnAlaThrGluValProIleSerGlnSerAspGlySerAlaValAlaIaIuThr	685
Db	2098	-----GTGACCTGCCCCGAGGGGAGCCAGTTCGGAAGGTTTCAGGCAACT	2145
OY	686	AsnThrIleAlaAsnGlnIleAsnThrAlaProIuYsProAlaAlaProThrIuThrLeuGln	705
Db	2146	-----CCCTCTTCTCAGCAACACAGTATGTGGAG	2175
OY	706	IleProProIuYsProAlaIleIuYsHisIleuProIuArgProGluThrIuHisProAsn	725
Db	2176	AGGCCACAGCTCTGCTATTTGTGACTCTTCGACTCCCGATGAGCGCCAC--TTC	2232
OY	726	ProAlaGlyLeuGlnGluSerIleSerAspValIuThrCysLeuValAlaSerIuGlu	745
Db	2233	CAGGCTGACCTGCAAGGCCCTTACCTGCAG-----	2262
OY	746	AsnValGlnValAlaGlnSerAsnLeuThrIuYsAspArgSerMetArgIuYsSerPheAsp	765
Db	2263	CGAATCTCCCCCGGCAG-----AGAGTGTACATCAG	2295
OY	766	MetGlyGlyGluThrLeuLeuSerValCysProMetValProIuYsAspLeuIuYsSer	785
Db	2296	CGAGACAGTGCACACCTCTGTCTCTG-----	2322

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QY      786  leuSeVValGlaHnuLeuIleatgSerThrGluGluAAsnIleGlnLeuSerGlySer  805
Db      2323  ATGTGCGTAAACAC-----GAGAGCTGGAGAGGTCTCCAAAGTGGCTTC  2367
QY      806  GluSerSerGlySerArgGlySerGlnAspPheTyro-----LysTyrParg  821
Db      2368  ACCATCTCCAGAGACAGAGATGATATTATGCTGGCCCCAATGGGGGGTGCAGCTGGATG  2427
QY      822  GluSerGluLeuPheLeuThrAspGluGluValGlyProGluGluThrGluThrAspThr  841
Db      2428  AGGAGACAAAGCGGTAAGTCTGCGCGAG-----GGTGAGACGACACAGACAGACGCCCC  2478
QY      842  phe 842
Db      2479  TTC 2481

RESULT 7
US-09-177-650-6
/ Sequence 6, Application US/09177650
/ Patent No. 6413719
/ GENERAL INFORMATION:
/ APPLICANT: Leppert, Mark F.
/ APPLICANT: Simoh, Nanda
/ APPLICANT: Charlier, Carole
/ TITLE OF INVENTION: KCNQ2 AND KCNQ3 - POTASSIUM CHANNEL GENES WHICH ARE
/ TITLE OF INVENTION: MUTATED IN BENIGN FAMILIAL NEONATAL CONVULSIONS (BFNC)
/ FILE REFERENCE: 2323-134
/ CURRENT APPLICATION NUMBER: US/09/177, 650
/ EARLIER FILING DATE: 1998-10-23
/ EARLIER APPLICATION NUMBER: 60/063, 147
/ NUMBER OF SEQ ID NOS: 129
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 6
/ LENGTH: 2914
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (19)..(2634)
/ FEATURE:
/ NAME/KEY: allele
/ LOCATION: (840)
/ OTHER INFORMATION: The polymorphism of a T to a C at this position
/ FEATURE:
/ NAME/KEY: mutation
/ LOCATION: (947)
/ OTHER INFORMATION: The missense mutation from a G to a T occurs at
/ FEATURE:
/ NAME/KEY: allele
/ LOCATION: (678)
/ OTHER INFORMATION: This position is polymorphic for C or T.
/ FEATURE:
/ NAME/KEY: allele
/ LOCATION: (750)
/ OTHER INFORMATION: This position is polymorphic for T or C.
/ FEATURE:
/ NAME/KEY: allele
/ LOCATION: (2598)
/ OTHER INFORMATION: This position is polymorphic for G or C.
/ NAME/KEY: allele
/ LOCATION: (2598)
/ OTHER INFORMATION: This position is polymorphic for T or C.
US-09-177-650-6

Alignment Scores:
Pred. No.:      5 5e-146      Length:      2914
Score:          1587.50      Matches:      366
Percent Similarity: 54.61%      Conservative: 106

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Best Local Similarity:	42.84%	Mismatches:	244
Query Match:	34.91%	Indels:	165
DB:	4	Gaps:	28

US-09-810-796-5 (1-888) x US-09-177-650-6 (1-2914)

OY	3	ASVAlGIsuSerGIYArGILyArGvAlLeuLeuAsnSerIAlAlArGvGIYASpGI	22
Db	163	GAGGTGGAGCA-----GTACCTTGCGCTCGGGGCGGAGCCGCAAAAGACGG	213
OY	23	LeuLeuLeuGIYhArGAlAlArhLeuGIYGIYGIYGIYGIYLeuArGIu	42
Db	214	ACCCGTCTCTG-----GAGCGGCGGCGCGGAGAGGGG	249
OY	43	SerArGArGIYLSGIInGIYAlArGMeSerLeuLeuGIYLS---ProLeuSerTYr	61
Db	250	CAGCGAGGAGACCCCGAGGGC-----ATCGGCTCTCTGGCCAAAGACCCCGCTAGCGCG	303
OY	62	ThrSerSerGIInSerCyArGArGAsnValLYSTyArGArGvAlGInAsnTYrLeuTYr	81
Db	304	CCAGTCAC-----AGAAACAAGGCCAAGACGGCGGCATCCAAACTTGATCTAC	354
OY	82	AsnValLeuGIuArProArGIYTTpAlArhLeIYrThIAlArhValPheLeuLeu	101
Db	355	GAGCCCTTGAGAGACCGGGGGCTGGCCCTGTTTACACAGGGTGGTTCCTGTAT	414
OY	102	ValPheGIYCySerLeuLeuSerValPheSerThrILleProGIuThISthLYSLeuAla	121
Db	415	GTCTGGGGGTCTGATTCCTGGCTGCTGACCACTTCAAGGAFATGAGACTGTCTCG	474
OY	122	SerSerCyLeuLeuLeuGIuPheValMetILeValValPheGIYLeuGIuPheIle	141
Db	475	GGAGACTGCTTCTGTACTGCGAGACATTTGCTATTTCATCTTGGAGCCGAGTTTCT	534
OY	142	ILearGIleTPSerAlaGIYCyScyCyArGTYArGvILYTPGIInGIYArGLeuArG	161
Db	535	TGAGGATCTGGCTCTGTGATGTGGCTGCGGATACAAAGCGCTGGCGGCGCACTYGAAG	594
OY	162	PheAlArILySproPheCySvAlILeAspThrILeValLeuILeAlSerILeAlVal	181
Db	595	TTTGGCAGGAGCGCCGTGCATGTGTGGACATCTTTGTCTGATTGCTCTGTGCGCACTG	654
OY	182	ValSerAlaLYSThrgInGIYAsnILePheAlaThrSerAlaLeuArGSerLeuArGPe	201
Db	655	GTTCGTGGGAAACAAGGCAATGTCTGAGCCACTCC---CTGGCAAGCCTGCGCTTC	711
OY	202	LeuGIInILeLeuArGMeValArGMeLAspArGArGIYhTrTPLYSLeuLeuGIY	221
Db	712	CTGCACATCTCGCATGTGCGGATGAGACCGGAGAGGTGCACCTTGAACTTGTGGGC	771
OY	222	SerValValTYrAlaHisSerLYSGLuLeuILeThrAlArTYrILeGIYpHeLeuVal	241
Db	772	TCAGCATGTGCTCCACACAAAGACATCATACGGGCTGTACATGCTTCTGTACA	831
OY	242	LeuILePheSerSerPheLeuValTYrLeuValGLuLYSAspAla-----	256
Db	832	CTTCATCTTCTTCATTTCTTGCTACTGGTTAGAAAGCGTCCACAGGTGATGCA	891
OY	257	-----AsnLYSGluPheSerThrTYrAlaAspAlaLeuTrTPILYThr	271
Db	892	CAMGAGAGAGATGAAGAGAGATTGAGACCTATGACATGCTGTGGGTGGGGCTCG	951
OY	272	ILeThrLeuThrThrILeGIYTYrGIYAspLYSThTrProLeuThrTPLeuGIYArGIu	291
Db	952	ATCACACTGGCCACCATATGGCTATGGAGACAAAGACCCAAACCTGGAAAGCGGTCTG	1011
OY	292	LeuSerAlaGIYpHeAlaLeuLeuGIYILeSerPhePheAlaLeuProAlaGIYLeu	311
Db	1012	ATTTGGCGGACCTTTTCCTTAATGAGGGTCCCTTTTGGCCCTTCCAGCGGCACTCTG	1071
OY	312	GIYSerGIYpHeAlaLeuLYSValGIInGIuInhSArGIInLYSHISpHeGIuLYSArG	331
Db	1072	GGGTGGGGGTGGCCCTTCAAGGTCCAGAGGACACACCTTCAGAAACCTTTGAGAAAAG	1131

OY		332	ArgAnSPRoVAlAAlAsnLeuIleGInCysValTTPArGSerTYrAlaLAspGIuLyS	351
Db	1132	AGGAACCGACGGCTGCAGACTCAATTAAGCTGCCCTGGAGGTATTATTCCTACCACCCCAAC	1191	
OY		352	SerValSer---LleAlatThrTrpLyS-----ProHisLeu	362
Db	1192	AGGATTGACCTGGTGCGCACATGGAGATTTTTGAAATCAGTGGTCHCTTTCTCTTCTTC	1251	
OY		363	LysAlaLeuHisThcCysSerProThraGInLyLSerPheLySGluAtgValAtG	382
Db	1252	AGGAAGAACAACCTGGAGGACACATCCACACCAAAGCTGGTCTTTGGATCGGGTTGCG	1311	
OY		383	MetAlaSerProArgGLyGInSerIleTyLSerSerArgInAlaSerValGIAspArgAtG	402
Db	1312	CTTTCTTAATCCCTGGTGGTAGCAATACTAAA-----GGAAAGCATATT	1353	
OY		403	SerProSerThraSPtleThraIleaglInLySerProThrLySaIGInLySerTrpSer	422
Db	1354	ACCCCTGCAATGATAGATGCCATAGAACAAAGACTCTTCTTAAGAACCAAAAGCCTGTGTGC	1413	
OY		423	PheAsnAspArgThrArgPheArgProSerLeuArgLeuLyS-----	436
Db	1414	TTAAACAAATAAAGACGTTTTCCGACGGCTTCCGGATGAACACCTACGCTTTCGGACG	1473	
OY		437	SerSerGlnProLySProValIleAspAlaSPthrAlaLeuGlYThrAspAspValTyR	456
Db	1474	AGTTCTGAA-----CATGCCGGGACAGGT-----GACCCCATGCGC	1509	
OY		457	AspGIuLySGlyCySGInCysAspValSerValGIuAspLeuthrProProLeuLySThr	476
Db	1510	GAAAGCAGGGCGTATGGAAATGACATTTCCCATGGAAGACATGATCCCCACCTGMAAGGC	1569	
OY		477	ValIleArgAlaIlleargIleMetLySPheHisValAlaLySarGlySPheLySGluThr	496
Db	1570	GCCATCCGAGCGGTGAGATTCTACATTCCTGCTGATATAAAAAAATTCAMAGGACACT	1629	
OY		497	LeuArgProTyTrAspValLyAspValIlleglInGlnTySerAlaGlnIleAspMet	516
Db	1630	TTCAGCGCCTTACCATGTGAAGGTGATGGACACATTCCTCCGGCATCTCGACATG	1689	
OY		517	LeucYSarGIleLySerLeuGlnThrArgValAlaSPGInIleLeuGlyLySGlnIle	536
Db	1690	CTTTCAGAGATTAAGTACCTTCAGACGAGATATGATATTTCACCCCTGGACCTGCC	1749	
OY		537	ThrSerAspLySLysSerArg-----	543
Db	1750	TCCACGCCCAAAACACAAGAACTCTGAAAGGCTCGACATTCACCTCCATCCATCCACAA	1809	
OY		544	-----GluLySIleThrAlaGlnHisGlnThrThr-----AspAspLeuSer	557
Db	1810	TCTCCCAAGAAATGAACCATATGTAGCCACACCATCCACATCAACAAATCGAAGCAAAAGC	1869	
OY		558	MetLeuGIARgValAlaLyLySaIGluLySGInValGInSerIleGInSerIleAsp	577
Db	1870	ATGATGGGAAAGTTGTAAAGTTGAAGACAGAGTTCCAGACATGGGGAAGAGCTGGAC	1929	
OY		578	CysLeuLeuAspIleTyrgInGlnValLeuArg-----	588
Db	1930	TTCCTCGTGAATTCGCACATGACACACATGAGAACGGTTGCAGGTGCAGTCCAGCATAT	1989	
OY		589	-----LysLySerAlaSerAlalaLeuAlaLeuAlaSerPheGlnIleProProPhe	605
Db	1990	TACCCACCAAGGACACTCCTCG-----CCAGGT	2019	
OY		606	GluCySGluGlnThrSerAspTYrGInSerProValAspSerLySaSpLeuSerLySer	625
Db	2020	GAAAGCAGAAAGAGAGGACACACAGGTATTCC--GATTGAAAAACATCATCTGCACAC	2076	
OY		626	AlaGlnAsnSerCIyLySLeuSerArgSerThrSerAlaSnIleSerArgGlyLeuGln	645
Db	2077	TATTCTGAGACAGGCCCCCGGAACACACCTTAAGCTTCCAC-----	2118	

Alignment Scores:

Pred. No.:	1,93e-109	Length:	900
Score:	1207.50	Matches:	227
Percent Similarity:	83.88%	Conservative:	28
Best Local Similarity:	74.67%	Mismatches:	40
Query Match:	26.56%	Indels:	9
DB:	4	Gaps:	2

US-09-810-796-5 (1-888) x US-09-105-058C-5 (1-900)

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QY 56 GLYLSProLeuSerYrTrhSerSerClnSerCysArGaArGaSnValLysYrArGArg 75
DB 13 GGGAAAGCCC-----CCGAAGCCCAAGCCCTTCTACCGCAAG 48
QY 76 ValGlnAsnTYrLeuTYrAsnValLeuGluArGProArGlyTrpAlaPheIleYrHis 95
DB 49 CTGCAGAAATTTCTCTACACAGCTGCTAGAGCGGCCCGCGCTGGCGTTCATCTACAC 108
QY 96 AlaPheValPheLeuLeuValPheGlyCysLeuIleLeuSerValPheSerThrIlePro 115
DB 109 GCCTACGTTCTCTTTAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 168
QY 116 GlnHisThrIleValAlaSerSerCysLeuLeuIleLeuGluPheValMetIleValVal 135
DB 169 GAGTACGACGAAGACTCTGAGGGGGCCCTTACATCTTGAAATGTGACTATCGTGGA 228
QY 136 PheGlyLeuGluPheIleIleArgIleTrpSerAlaGlyCysCysArGTrpYrArgIly 155
DB 229 TTGCGTGTGAGTACTTGTGAGGATCTGGGCTGCGAGCTGCTGTTGCCGATACGAGGC 288
QY 156 TrpGlnIlyArGLeuArGpHeAlaArgIlyProPheCysValIleAspThrIleValLeu 175
DB 289 TGGAGGGGCGAGCTCAAGTTGGCCAGGAAGCGTCTGTGTGATGATATCATGTGIGCTG 348
QY 176 IleAlaSerIleAlaValAlaSerAlaLysThrGlnGlyAsnIlePheAlaThrSerAla 195
DB 349 ATTGCCCTCCATGTGCTGCTGCTGCTGCTGCCAGGGAATGCTTTGCCACATCTGCG 408
QY 196 LeuArGSerLeuArGpHeLeuGlnIleLeuArGMetValArGMeAspArGArgIlyGly 215
DB 409 CTTCGGAGCTTGCCTGCTCTTCCAAATCTTGGGATGATCCGATGACCGAGGGGTGCG 468
QY 216 ThrTrpLysLeuLeuGlySerValValTYrAlaHisSerLysGluLeuIleThrAlaTrp 235
DB 469 ACCGGAAGCTCTTGGATCGGTACTTACGCTCACAGCAAGAGAGCTGTGACTGCTGG 528
QY 236 TYrIleGlyPheLeuValLeuIlePheSerSerPheLeuValTYrLeuValGluIlyAsp 255
DB 529 TACATTTGGCTTCTCTGCTCATCTGCGCTCATTTCTGCTACTTGGCAAAAGGGGT 588
QY 256 AlaAsnLysGluPheSerThrTYrAlaAspAlaLeuTrpTrpGlyThrIleThrIleThr 275
DB 589 GAGATATGACCACTTTGACACCTTACAGACATGACCTGTGGGGCTGTGACCTGAGG 648
QY 276 ThrIleGlyTYrGlyAspLysThrProLeuThrTrpLeuGlyArGLeuLeuSerAlaGly 295
DB 649 ACCATTGGCTACGGGACAAAGTACCTCAGACCTGGAAGGAGAGGTGCTGGCAGGAC 708
QY 296 PheAlaLeuLeuGlyIleSerPhePheAlaLeuProAlaGlyIleLeuGlySerGlyPhe 315
DB 709 TTTACCTCATTTGGTGTCTGTTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 768
QY 316 AlaLeuLysValGlnGluGlnHisArGlnLysHisPheGlnLysArGArgAsnProAla 335
DB 769 GCCCTGAAAGTCCAGACAGCATGCGCAAAACATTTTGAAGAAAGGGGGAACCTTGG 828
QY 336 AlaAsnLeuIleGlnIlyCysValTrpArGSerTYrAlaAlaAspGluLysSerValSerIle 355
DB 829 GCAAGTCTGATCTCACTGTGCTGAGATTTCTATGCTACTAACCTTCACAGCACCGACTG 888
QY 356 ---AlaThrTrp 358
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DB 889 CACTCCAGCTGG 900

RESULT 10

US-09-105-058C-3

/ Sequence 3, Application US/09105058C

/ Patent No. 6403360

/ GENERAL INFORMATION:

/ APPLICANT: Blamar, Michael A.

/ APPLICANT: Dworetzky, Steven

/ APPLICANT: Gruboff, Valentin K.

/ APPLICANT: Levesque, Paul C.

/ APPLICANT: Little, Wayne A.

/ APPLICANT: Neubauer, Michael G.

/ APPLICANT: Yang, Wen-Pin

/ TITLE OF INVENTION: KONO POTASSIUM CHANNELS AND METHODS OF MODULATING SAME

/ FILE REFERENCE: 3053-4052

/ CURRENT APPLICATION NUMBER: US/09/105,058C

/ CURRENT FILING DATE: 1998-06-26

/ PRIOR APPLICATION NUMBER: US 60/055,599

/ PRIOR FILING DATE: 1997-08-12

/ NUMBER OF SEQ ID NOS: 28

/ SOFTWARE: PatentIn Ver. 2.1

/ SEQ ID NO 3

/ LENGTH: 900

/ TYPE: DNA

/ ORGANISM: Homo sapiens

/ FEATURE:

/ OTHER INFORMATION: 900 nucleotides of human KCNQ2

US-09-105-058C-3

Alignment Scores:

Pred. No.:	7.52e-109	Length:	900
Score:	1201.50	Matches:	226
Percent Similarity:	83.55%	Conservative:	28
Best Local Similarity:	74.34%	Mismatches:	41
Query Match:	26.42%	Indels:	9
DB:	4	Gaps:	2

US-09-810-796-5 (1-888) x US-09-105-058C-3 (1-900)

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QY 56 GLYLSProLeuSerYrTrhSerSerClnSerCysArGaArGaSnValLysYrArGArg 75
DB 13 GGGAAAGCCC-----CCGAAGCCCAAGCCCTTCTACCGCAAG 48
QY 76 ValGlnAsnTYrLeuTYrAsnValLeuGluArGProArGlyTrpAlaPheIleYrHis 95
DB 49 CTGCAGAAATTTCTCTACACAGCTGCTAGAGCGGCCCGCGCTGGCGTTCATCTACAC 108
QY 96 AlaPheValPheLeuLeuValPheGlyCysLeuIleLeuSerValPheSerThrIlePro 115
DB 109 GCCTACGTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 168
QY 116 GlnHisThrIleValAlaSerSerCysLeuLeuIleLeuGluPheValMetIleValVal 135
DB 169 GAGTATGAGGAAGCTTGGAGGGGGCCCTTACATCTGGAATGTGACTATCTGCTG 228
QY 136 PheGlyLeuGluPheIleIleArgIleTrpSerAlaGlyCysCysArGTrpYrArgIly 155
DB 229 TTTCGCTGAGTACTTCTCTGCGGATCTGCGGCGCAGGCTGCTGCGGAGCGTGGC 288
QY 156 TrpGlnIlyArGLeuArGpHeAlaArgIlyProPheCysValIleAspThrIleValLeu 175
DB 289 TGGAGGGGCGGCTCAAGTTTGGCCGGAACCTCTCTGTGATTTGACATCATGTGCTCT 348
QY 176 IleAlaSerIleAlaValAlaSerAlaLysThrGlnGlyAsnIlePheAlaThrSerAla 195
DB 349 ATCCCTTCATTTGGGTCTGCGCGCGCTCCAGAGGCAACGTTTGGCAACATCTGCG 408
QY 196 LeuArGSerLeuArGpHeLeuGlnIleLeuArGMetValArGMeAspArGArgIlyGly 215
DB 409 CTTCGGAGGCTTGCCTTCTCTCAGATTTCTGCGATGATCCGATGAGCGGGGAGGAGC 468
QY 216 ThrTrpLysLeuLeuGlySerValValTYrAlaHisSerLysGluLeuIleThrAlaTrp 235

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Db 469 ACCTGAGAGCTGGGCTGCTGTCATGCCCCAGACAGAGACTGCTGCTGCTG 528
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Qy 236 TyrIleGlyPheLeuValIlePheSerSerPheLeuValTyrLeuValGlyLysasp 255
|||||
Db 529 TACATGGCTCTCTTCTGTCATCTGACCTGCTGCTGCTGCTGCTGCTGCTG 588
|||
Qy 256 AlaAsnLysGluPheSerTrpTyrAlaAspAlaLeuTrpTrpGlyThrIlePheLeuThr 275
|||||
Db 589 GAGACAGACACTTGTGACACTACGCGGATGCTGCTGCTGCTGCTGCTGCTGAC 648
|||
Qy 276 ThrIleGlyTyrGlyAspLysTyrProLeuThrTrpLeuGlyArgLeuLeuSerIleagly 295
|||||
Db 649 ACCATTGGCTACGCGGAGCAAGTACCCAGACCTGGAACGCGACGCTGCTGCGCAACC 708
|||
Qy 296 PheAlaLeuGlyLysSerPhePheAlaLeuProAlaGlyIleLeuGlySerIlyPhe 315
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Db 709 TTACACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 768
|||
Qy 316 AlaLeuLysValGlnGlnGlnHisArgGlnLysHisPheGlnLysArgArgAsnProAla 335
|||||
Db 769 GCCCTGAAGGTTGAGGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 828
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Qy 336 AlaAsnLeuIleGlnGlyValITrpaGlySerTyrAlaAlaAspGluLysSerValSerIle 355
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Db 829 GAGGCTGATGTCAGTCGCGCTGAGATTACCCACCAACCTCTGCGCAGACAGACTG 888
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Qy 356 ---AlaThrTrp 358
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Db 889 CACTCCACGCTGG 900
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RESULT 11
us-09-135-021-1
; Sequence 1, Application us/09135021A
; Patent No. 6150104
; GENERAL INFORMATION:
; APPLICANT: Splawski, Igor
; APPLICANT: Keating, Mark T.
; TITLE OF INVENTION: A HOMOZYGOUS MUTATION IN KVLQTL WHICH CAUSES JERVELL,
; FILE REFERENCE: 2323-128
; CURRENT FILING DATE: 1998-08-17
; EARLIER FILING DATE: 1998-07-29
; EARLIER FILING DATE: 1997-06-13
; EARLIER APPLICATION NUMBER: 60/094,477
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 3181
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (163)..(2190)
us-09-135-021-1

Alignment Scores:
Pred. No.: 1.6e-99 Length: 3181
Score: 1116.50 Matches: 294
Percent Similarity: 52.75% Conservative: 118
Best Local Similarity: 37.64% Mismatches: 247
Query Match: 24.55% Indels: 122
DB: 3 Gaps: 23

US-09-810-796-5 (1-888) x us-09-135-021-1 (1-3181)

Qy 7 GlyArgGlyArgValLeu---LeuAsnSerAlaAlaAlaArgGlyAspGlyLeuLeu 25
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Db 189 GCGCCAGAGGAAAGCCCTGGGGGCGCGCTCGCAGCGCGCGCGCGCGCGCGCGG 248
|||||
Qy 26 LeuGlyThrArgAlaAlaAlaThrLeuGlyGlyGlyGlyGlyGlyLeuArgLysSerArgArg 45
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Db 249 CTTGGCCAGAGACTGCCCTTCTCTGCTGAGCTGGCGGAGGCGCGCGCGCGCGCG 308
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Qy 46 GlyLysGlnGlyAlaArgMet----- 52
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Db 309 GCTCTACAGCCCATGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 368
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Qy 53 -----SerLeuLeuGlyLysProLeu-Se 60
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Db 369 GCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 428
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Qy 60 rTyrTrpSerSerGlnSerCysArgArgAsnValLysTyrArg---ArgValGlnAsnTy 79
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Db 429 GCGCGCTCTCATTTACAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 488
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Qy 79 rLeuTyrAsnValLeuGlnArgProArgLysTrp---AlaPheIleTyrHisAlaPheVa 98
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Db 489 CGTCTACAACTTCTCGAGCGTCCACCGCGCTGGAATGCTTCGTTTACCACTTCGCGCT 548
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Qy 98 lPheLeuLeuValPheGlyCysLeuIleLeuSerValPheSerThrIleProGluHisTh 118
|||||
Db 549 CTTCTCATGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 608
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Qy 118 rLysLeuAlaSerSerCysLeuLeuIleLeuGlnPheValMetIleValValPheGlyLe 138
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Db 609 CGCCCTGGCGACGCGGAGCTCTTCTTGATGAGATGCTGCTGCTGCTGCTGCTGCTG 668
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Qy 138 uGluPheIleIleArgIleTrpSerAlaGlyCysCysArgTyrArgLysTrpGlnI 158
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Db 669 GAGTACGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 728
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Qy 158 rArgLeuArgPheAlaArgLysProPheCysValIleAspThrIleValLeuIleAlaSe 178
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Db 729 GCGGCTGCGCTTGGCCGGAAGGCCATTTCATCATCATGACCTGATGCTGCTGCTG 788
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Qy 178 rIleAlaValAlaSerAlaLysThrGlnGlnAsnIlePheAlaThrSerAlaLeuArgSe 198
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Db 789 CATGGGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 848
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Qy 198 rLeuArgPheLeuGlnIleLeuArgMetValAlaArgMetAspArgArgGlyLysThrTrpLy 218
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Db 849 CATCGGCTCTGCAAGATCTGAGAGTGTACAGCTGCAAGCGCGAGGAGGACCTGAG 908
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Qy 218 sLeuLeuGlySerValValTyrAlaHisSerLysGluLeuIleThrAlaTrpTrpIleG 238
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Db 909 GCTCTGCGCTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 968
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Qy 238 rPheLeuValLeuIlePheSerSerPheLeuValTyrLeuValGlyLysAspAla----- 256
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Db 969 CTTCTGGGCTCATCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1028
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Qy 257 -----AsnLysGluPheSerThrTyrAlaAspAlaLeuTrpTrpGlyThrIleTh 273
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Db 1029 CGAGTCAGCGCGCGGAGTTGGAGCTTGGCAGCTACGAGATGCGCTGCTGCTGCTGCTG 1088
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Qy 273 rLeuThrThrIleGlyTyrGlyAspLysThrProLeuThrTrpLeuGlyArgLeuLeuSe 293
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Db 1089 AGTCACCAACATCGGCTATGGGAGACAAGTCCGCCACAGCTGCTGCTGCTGCTGCTG 1148
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Qy 293 rAlaGlyPheAlaLeuLeuGlyIleSerPhePheAlaLeuProAlaGlyIleLeuGlySe 313
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Db 1149 CTTCTGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1208
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Qy 313 rGlyPheAlaLeuLysValGlnGlnHisArgGlnLysHisPheGluLysArgArgAs 333
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Db 1209 GGGGTTTCCCTGAAGGTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGATCC 1268
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Qy 333 nProAlaAlaAsnLeuIleGlnGlyValITrpaGlySerTyrAlaAlaAspGluLysSerVa 353
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Db 1269 GCGCGACGCTCATCATTTACAGCCGATGAGAGTGTATGCTGCGGAGAACCCGACATC 1328
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Qy 353 lSerIleAlaThrTrpLysProHisLeuLysAlaLeu-----HisThr---CysSe 369
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Db 1329 CTCCTGAGAGATCTACATCCGAGAGGCCCCCGGAGCCACACTCTGCTCTC 1382
OY rProthrasnGlnLysLeuSerPheLysGluArgMetAlaSerProArgLysG1 389
1383 ACCGACCCCAAGCC-----AAGAGTCTGTGTGTAAAGAAAAAAGTTCAA 1433
OY nSerLLeuSerArgGlnAlaSerValGlyAspArgArgSerProSerThrAspLLeu 409
1434 GCTGACACAAAGACATGGGTGCTCTGAGAGAGATGCTCAAGTCCCATATATAC 1493
OY rAlaGluGlySerProThrLysValGlnLysSerTrpSer-----PheAsnAspAr 426
1494 GTCCGACCCCGGAGAGAGGCGGCGCTGGACACTCTCTCTCCAGCGCTATGACAGTTC 1553
OY gThrArgPheArgProSerLeuArgLeuLysSerSerGlnProLysProValLLeaSpAl 446
1554 TGTAGAGAGAGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1596
OY 446 aAspThrAlaLeuGlyThrAspAspValTyrAspLLeuLysGlyGlnLysAspValSe 466
1597 -----TTTCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1637
OY rValGluAspLeuThrProProLeu-----LysThr 476
1638 AGGGGAGACTCTGCTGACACCCCATCCACAGCTCGGAGAGAGAGAGAGAGAGAGAG 1697
OY rValLLeaArgAlaLLeaArgLLeuMetLysPheHisValAlaLysArgLysPheLysGluTh 496
1698 CACCATTAAGGTCAATTCAGACAGCATGACTTGTGGCCAAAGAAATTCACAGCAAC 1757
OY rLeuArgProThrArgProLysAspValLLeuGlnLysSerAlaGlyHisLeuAspMe 516
1758 GCGGAGAGCTTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1817
OY tLeuCyArgGlyLeuSerLeuGlnThrArgValAspGlnLeuGlyLysGlyLysL 535
1818 CATGTGCGGATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1877
OY 536 -----LLeuThrSerAspLysLysSerArgLLeuLysLLeuThrAlaGlnLysGlnThrThrs 554
1878 GTTCATCTCCCTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1913
OY 554 pAspLeuSerMetLeuGlyArgValValLysValGlnLysGlnLysLLeuSerLLeuSe 574
1914 CAGCAACAGATCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1973
OY rLysLeuAspCysLeuLeuAspLLeuArgLLeuGlnValLeuArgLysGlySerAlaSerA 594
1974 GAGCTGCGCATCATCACCGACATGCTTCCAGCGTCTCTCCAGCGTCCAGCGAGCAG 2033
OY 594 lAlaLeuAlaLeuAlaSerPheGlnLLeuProProPheGlnLysGlnLysGlnLys 614
2034 CCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 2084
OY lInsProValAspSer-----LysAspLeuSerGlySerAlaGlnAsnSerGlyCysLeu 632
2085 CTGCGGCGAGTGGCGGCTCCGTGACCTTACGCTCTCTCCAGCAACAGAGAGAGAGAG 2144
OY 633 SerArgSerThrSer-----AlaAsnLLeuSerArgLLeu 644
2145 CTACAGCAGCAGTACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2204
OY 645 GlnPheLLeuThrProAsnGlnLysSerAlaGlnThrPhe-----TyrAlaLeuSer 662
2205 GCGTGGGAGTGGCGGCTGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2264
OY 663 ProThrMetHis-----SerGlnAlaThrGlnValProLLeuSerGlnAspGly 679
2265 GAGGAGAGCGCACTCTCTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2315
OY 680 SerAlaValAlaAlaThrAsnThrLLeuAlaAsnGlnLLeuAsnThrAlaProLysProAla 699
2316 -----GCCCAATAATCCCAT 2330

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OY 700 AlaProThrThrLeuGlnLLeuPro-----ProProLeuPro 711
Db 2331 GAGCCAGTGTCTGTGGCAGACCTTGACACTTGGGGGCTCAGCAAGAGCCACTTCT 2387

RESULT 12
US-09-135-020-1
Sequence 1, Application US/09135020
Patent No. 6274332
GENERAL INFORMATION:
APPLICANT: Keating, Mark T.
APPLICANT: Sanguinetti, Michael C.
TITLE OF INVENTION: MUTATIONS IN THE KCNE1 GENE ENCODING HUMAN MINK WHICH
TITLE OF INVENTION: CAUSE ARRHYTHMIA SUSCEPTIBILITY THEREBY ESTABLISHING
FILE REFERENCE: 2323-131
CURRENT APPLICATION NUMBER: US/09/135,020
EARLIER FILING DATE: 1998-08-17
EARLIER APPLICATION NUMBER: 08/921,068
EARLIER FILING DATE: 1997-08-29
EARLIER APPLICATION NUMBER: 08/739,383
EARLIER FILING DATE: 1996-10-29
EARLIER APPLICATION NUMBER: 60/019,014
EARLIER FILING DATE: 1995-12-22
EARLIER APPLICATION NUMBER: 60/094,477
NUMBER OF SEQ ID NOS: 114
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 3181
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (163)..(2190)
US-09-135-020-1

Alignment Scores:
Pred. No.: 1 6e-99 Length: 3181
Score: 1116.50 Matches: 294
Percent Similarity: 52.75% Conserved: 118
Best Local Similarity: 37.64% Mismatches: 247
Query Match: 24.55% Indels: 122
DB: 4 Caps: 23

US-09-810-796-5 (1-888) x US-09-135-020-1 (1-3181)
OY 7 G1YArgG1YArgValLLeu--LLeuAsnSerAlaAlaAlaArgG1YAspG1YLeuLeuLeu 25
189 GCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 248
OY 26 LeuG1YThrArgAlaAlaThrLeuG1YG1YG1YG1YG1YLeuArgG1YLeuArgArg 45
249 CTTGGCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 308
OY 46 G1YsGlnG1YAlaArgMet----- 52
309 GCTTACGCGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 368
OY 53 -----SerLeuLeuG1YLysProLeu--Se 60
369 GCCCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 428
OY 60 rTyrThrSerSerGlnSerCysArgArgAsnValLysTyrArg--ArgValGlnAsnTyr 79
429 GCGGCTCTCCATCTACACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 488
OY rLeuTyrAsnValLeuG1YArgProArgLysTyr--AlaPheLLeuTyrHisAlaPheVa 98
489 GGTCTACACTTCTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 548
OY 98 lPheLeuLeuValPheG1YCysLeuLLeuSerValPheSerThrLLeuProLysHisTh 118

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; CURRENT FILING DATE: 1998-08-17
 ; PRIOR APPLICATION NUMBER: 60/094,477
 ; PRIOR FILING DATE: 1998-07-29
 ; PRIOR APPLICATION NUMBER: 08/7921,068
 ; PRIOR FILING DATE: 1997-08-29
 ; PRIOR APPLICATION NUMBER: 08/739,383
 ; PRIOR FILING DATE: 1996-10-29
 ; PRIOR APPLICATION NUMBER: 60/019,014
 ; PRIOR FILING DATE: 1995-12-22
 ; NUMBER OF SEQ ID NOS: 116
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 1
 ; LENGTH: 3181
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (163)..(2190)
 ; US-09-135-010A-1

Alignment Scores:
 Pred. No.: 1,6e-99 Length: 3181
 Score: 1116.50 Matches: 294
 Percent Similarity: 52.75% Conservative: 118
 Best Local Similarity: 37.64% Mismatches: 247
 Query Match: 24.55% Indels: 122
 DB: Gaps: 23

US-09-810-796-5 (1-888) x US-09-135-010A-1 (1-3181)

Oy 7 gLyArggLyArgValLeu--LeuAsnSerAlaAlaAlaArgGlyAspGlyLeuLeu 25
 Db 189 GCGCGAGAGAGAGAGCGCTGGGGTGGGGCGCGCCGCGAGCGCGCGCGCGCGCGCGCGCG 248
 Oy 26 LeuGlyThrArgAlaAlaAlaThrLeuGlyGlyGlyGlyGlyLeuArgGlySerArgArg 45
 Db 249 CCGGCGAAGAGAGTCCCTCTCTGCTGGAGCTGGCGGAGGCGCGCGCGCGCGCGCGCGCG 308
 Oy 46 gLyArgGlyAlaArgMet----- 52
 Db 309 GCTCTACCGCGCGCATCG 368
 Oy 53 -----SerLeuGlyLysProLeu-Se 60
 Db 369 GCCCG 428
 Oy 60 rTyThrSerGlnSerArgArgAsnValLysTyrArg--ArgValGlnAsnTyr 79
 Db 429 GCGCGCTCCATCTACACAGCG 488
 Oy 79 rLeuTyrAsnValLeuGlyArgProArgGlyTyrP--AlaPheIleTyrHisAlaPheVa 98
 Db 489 CGCTCAACATCTTCGAGCG 548
 Oy 98 lPheLeuValPheGlyCysLeuIleLeuSerValPheSerThrIleProGluHisTh 118
 Db 549 CTTCCTCATCTCTGCTGCT 608
 Oy 118 rLysLeuAlaSerSerGlyLeuIleLeuGluPheValMetIleValValPheIleLys 138
 Db 609 CGCGCTGCG 668
 Oy 138 uGluPheIleIleArgIleTyrPserAlaGlyCysCysCysArgTyrArgGlyTyrPIngl 158
 Db 669 GGAATAGCTGCTCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 728
 Oy 158 yArgLeuArgPheAlaArgLysProPheCysValIleAspThrIleValLeuIleAlaSe 178
 Db 729 GCGCGCTCGCGCTTCGCGGAGGCCATTTCCATCATCATCATCATCATCATCATCATCATCAT 788
 Oy 178 rIleAlaValAlaSerAlaLysThrGlnGlyAsnIlePheAlaThrSerAlaLeuArgSe 198
 Db 789 CATGGTGTCTCTGCGTGGCGCTCCAAAGGGCAGGAGTGTGGCAGCTGCGCATCAGGGG 848

Oy 198 rLeuArgPheLeuGlnIleLeuArgMetValArgMetAspArgArgGlyThrTrrLy 218
 Db 849 CATCGCTCTTCGAGATCTGAGATGCTACACCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 908
 Oy 218 sLeuLeuGlySerValValTyrAlaHisSerLysGluLeuIleThrAlaTrrTrrLecI 238
 Db 909 GCTCTGGGCTCCGCGGCTTCATCATCACCGCGCGAGAGCTGATACACCTGCTACATCGG 968
 Oy 238 yPheLeuValLeuIlePheSerSerPheLeuValTyrLeuValGluLysAspAla----- 256
 Db 969 CTCTCGGCGCTCATCT 1028
 Oy 257 -----AsnLysGluPheSerThrTyrAlaAspAlaLeuTrrPrrLyThrIleTh 273
 Db 1029 CGAGTCAGCGCGCGGTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1088
 Oy 273 rLeuThrThrIleGlyArgGlyAspLysThrProLeuThrTrrPrrLyArgLeuLeuSe 293
 Db 1089 AGTCACACCATCGGCTATGGGGACAGAGTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1148
 Oy 293 rAlaGlyPheAlaLeuLeuGlyLysSerPhePheAlaLeuProAlaGlyIleLeuGlySe 313
 Db 1149 CTCTGCT 1208
 Oy 313 rGlyPheAlaLeuLysValGlnGlnGlnHisArgGlnLysHisPheGluLysArgArgAs 333
 Db 1209 GGGGTTCCTCGAAGCTGACAGCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1268
 Oy 333 nProAlaAlaAsnLeuIleGlnCysValTrrPrrSerThrAlaAlaAspGluLysSerVa 353
 Db 1269 GGGCGAGACCTCATCTATTCAGCGCATGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1328
 Oy 353 lSerIleAlaThrTrrLysProHisLeuLysAlaLeu-----HisThr--CysSe 369
 Db 1329 CTCC-----ACCTGGAAGATCTACATCCGGAAGGCGCGCGGAGCACACTCTGCTGTC 1382
 Oy 369 rProThrAsnGlnLysLeuSerPheLysGlyArgValArgMetAlaSerProArgGlyGl 389
 Db 1383 ACCGAGCGCGCAAGCC-----AAGAGCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1433
 Oy 389 nSerIleSerArgGlnAlaSerValGlyAspArgArgSerProSerThrAspIleTh 409
 Db 1434 GGTGACAAAGACATGAGGAGTCTCTGAGAGAGAGATGTCAACATGCCCATATATCAC 1493
 Oy 409 rAlaGluGlySerProThrLysValGlnLysSerTrrSer-----PheAsnAspAr 426
 Db 1494 GTGGACCGCGCGCAAGAGCGCGCGGTGGACCACTCTCTCTCTCTCTCTCTCTCTCTCTCT 1553
 Oy 426 gThrArgPheArgProSerLeuArgLeuLysSerSerGlnProLysProValIleAspAl 446
 Db 1554 TGTAGAGAGAGCGCAACACTG---CTGGAAGTGAAGCATGCGCCCAT----- 1596
 Oy 446 aAspThrAlaLeuGlyThrAspAspValTyrAspGluLysGlyCysGlnCysAspValSe 466
 Db 1597 -----TTCATGAGAACCAACACCTTGCGCGAGAGAC-----CTGGACCTGGA 1637
 Oy 466 rValGluAspLeuThrProProLeu-----LysTh 476
 Db 1638 AGGGAGACACTCTGTCACACCATCACCATCTCACAGCTGCGGGAACACCATCGGGG 1697
 Oy 476 rValIleArgAlaIleArgIleMetLysPheHisValAlaLysArgLysPheLysGluTh 496
 Db 1698 CACCATTAAGGTCTTTCGAGCGATGCAGTACTTGTGTGGCAAGAAATTCACGCAAGC 1757
 Oy 496 rLeuArgProTyrAspValLysAspValIleGluGluTyrSerAlaGlyHisLysAspMe 516
 Db 1758 GCGGAACCTTAGATGTGGGAGCGATTCATGACAGTACAGGCGCACCTCATCACT 1817
 Oy 516 tLeuCysArgIleLysSerLeuGlnThrArgValAspGlnIleLeuGlyGlyGln-- 535
 Db 1818 CATGGTGGCATCAGAGAGCTGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1877

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QY 536 ----lIeThSerAspLysSerArgGluLyslIeThraLagluHsIuThrThras 554
      |||::: |||:::|||||:::|||||:::
Db 1878 GTTCATCTCCGCTCTCAAGAAAGACAGATCGC-----GG 1913
QY 554 paspleuSerMetleuclArgValValLysValGluLysGlnValGlnSerIleGluSe 574
      |||::: |||:::|||||:::|||||:::
Db 1914 CACCAACACGATCGGGCCGCCCGCAAGACGAGTGAAGACAGAGGAGCAGCTGACCA 1973
QY 574 rLysleuAspCysleuLeuAspIleTyrgInlValleuArgLysGlySer-AlaseRa 594
      |||::: |||:::|||||:::|||||:::
Db 1974 GAGCTGGCACTCATCCGACATGCTTCACACGCTGCTTCCTTCAGCGGTGAGGAC 2033
QY 594 lAleuAlaleuAlaseRPhelGlnlIleProPhelGluCysGluClnIhRserAspTyrg 614
      |||::: |||:::|||||:::|||||:::
Db 2034 CCCCAGGAGGGGGGCC-----CCCCAGAGAGGGGGGGGCCCATTCACCCAGCC 2084
QY 614 lInserProValaspSer---LysAspleuSerGlySer-AlaGlnAsnSerclYcysleu 632
      |||::: |||:::|||||:::|||||:::
Db 2085 CTCGCGCAGTGGCGGCGCTCGTCGACCTGAGCTCTCTCGCCAGACACACCTGCCAC 2144
QY 633 SerArgSerThrSer-----AlaAsnIleSerArgGlyleu 644
      |||::: |||:::|||||:::|||||:::
Db 2145 CTACGACACTGACCTGACCGCCAGAGAGGGGCCCGAGTAGGGGCTGAGAGGGGATGG 2204
QY 645 GlNpheIleuThrProAsnGluPheSerAlaGlnIhRphe-----TyrAlaleuSer 662
      |||::: |||:::|||||:::|||||:::
Db 2205 GGGTGGGGGATGGGCTGAGTGAAGAGGGGAGGCCAAGAGTGGCCCTGAGCTCTCT 2264
QY 663 ProThrMetHis-----SerGlnAlaThrgInValProIleSerclYcysleu 679
      |||::: |||:::|||||:::|||||:::
Db 2265 GAGGAGGAGCCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2315
QY 680 SerAlaValAlaIhRAsnThrIleAlaAsnGlnIleAsnThrAlaProLysProAla 699
      |||::: |||:::|||||:::|||||:::
Db 2316 -----GCCCATTCATCCCAT 2330
QY 700 AlaProThrThreugInlIlePro-----ProProleuPro 711
      |||::: |||:::|||||:::|||||:::
Db 2331 GAGCAATGCTGCTGAGACAGCTGCACTTGCGGGCTCAGCAAGGCCACCTCTTCT 2387

RESULT 14
US-09-444-871-1
; Sequence 1, Application us/09444871
; Patent No. 6323026
; GENERAL INFORMATION:
; APPLICANT: Keating, Mark T.
; APPLICANT: Sanguinetti, Michael C.
; TITLE OF INVENTION: MUTATIONS IN THE KCNE1 GENE ENCODING HUMAN MINK WHICH
; TITLE OF INVENTION: CAUSE ARRYTHMIA SUSCEPTIBILITY THEREBY ESTABLISHING
; FILE REFERENCE: 2323-131
; CURRENT APPLICATION NUMBER: US/09/444,871
; EARLIER FILING DATE: 1999-11-22
; EARLIER APPLICATION NUMBER: US 09/135,020
; EARLIER FILING DATE: 1998-08-17
; EARLIER APPLICATION NUMBER: 08/921,068
; EARLIER FILING DATE: 1997-08-29
; EARLIER APPLICATION NUMBER: 08/739,383
; EARLIER FILING DATE: 1996-10-29
; EARLIER APPLICATION NUMBER: 60/019,014
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 60/094,477
; EARLIER FILING DATE: 1998-07-29
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: Patent Ver. 2.0
; SEQ ID NO 1
; LENGTH: 3181
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (163)..(2190)

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US-09-444-871-1
Alignment Scores:
Pred. No.: 1,6e-99 Length: 3181
Score: 1116.50 Matches: 294
Percent Similarity: 52.75% Conservative: 118
Best Local Similarity: 37.64% Mismatches: 247
Query Match: 24.55% Indels: 122
DB: 4 Gaps: 23

US-09-810-796-5 (1-888) x US-09-444-871-1 (1-3181)
QY 7 GLYArgGlyYArgValleu---leuAsnSerAlaAlaAlaArgGlyAspGlyLeuLeu 25
      |||::: |||:::|||||:::|||||:::
Db 189 GGGCGAGAGAGAGAGCGCTGGGTTGGGGCCGCTGCAGGCGCCCCGGGGGAGCGCGG 248
QY 26 leuGlyThrArgAlaAlaIhRleuGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 45
      |||::: |||:::|||||:::|||||:::
Db 249 CCGGCCAAGAGATGGCCCTTCGCTGAGAGTGGCGAGGGGCGCGCGCGCGCGCGCG 308
QY 46 GlyLysGlnGlyAlaArgMet----- 52
      |||::: |||:::|||||:::|||||:::
Db 309 GCTTACGCGCCCATGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 368
QY 53 -----SerleuLeuGlyLysProleu-Se 60
      |||::: |||:::|||||:::|||||:::
Db 369 GCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 428
QY 60 rTyrrhSerSerclInserCysArgArgAsnValLysTyArg---ArgValGlnAsnTy 79
      |||::: |||:::|||||:::|||||:::
Db 429 GCGCGCTCATCTACAGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 488
QY 79 rleuTyraSnValleuGluArgProArgGlyTrp---AlaPheIleTyrrhAlaPheVa 98
      |||::: |||:::|||||:::|||||:::
Db 489 CGCTTCACTCTCTCTGAGGCTGCCACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 548
QY 98 lPheleuLeuValPheGlyCysleuIleleuSerValPheSerThrlIleProGluHsTh 118
      |||::: |||:::|||||:::|||||:::
Db 549 CTTCCTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 608
QY 118 rLysleuAlaSerSerCysleuLeuIleleuGluPheValMetIleValAlaPheGlyLe 138
      |||::: |||:::|||||:::|||||:::
Db 609 CGCCCTGCGCCAGCGGAGCTCTCTCTGAGAGAGATGCTGCTGCTGCTGCTGCTGCTG 668
QY 138 uGluPheIleIleArgIleThrPheSerAlaGlyCysCysArgTyArgGlyTrpGlnI 158
      |||::: |||:::|||||:::|||||:::
Db 669 GGAATGAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 728
QY 158 YArgLeuArgPheAlaIhRArgLysProphecysValIleAspThrlIleValleuAlaSe 178
      |||::: |||:::|||||:::|||||:::
Db 729 GCGGCTGCGCTTGGCGCGGAGCCCATTTCCATCATGACCTCATGCGTGTGCGGCTC 788
QY 178 rIleAlaValAlaSerAlaLysThrgInGlyAsnIlePheAlaThrSerAlaLeuArgSe 198
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Db 789 CATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 848
QY 198 rleuArgPheleuGlnIleleuArgMetValArgMetAspArgGlyGlyTrpLys 218
      |||::: |||:::|||||:::|||||:::
Db 849 CATCGCTTCTCTGAGATCTCTGAGAGATGCTACAGTGCAGCGGAGGAGGAGGAGGAG 908
QY 218 sLeuLeuGlySerValValTyrrhAlaHisSerLysGluLeuLeuThraLarTPyrrIleG 238
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Db 909 GCGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 968
QY 238 yPheleuValleuIlePheSerSerPheleuValTyrrhValGlnLysAspAla----- 256
      |||::: |||:::|||||:::|||||:::
Db 969 CTTCCTGCGGCTCATCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1028
QY 257 -----AsnLysGluPheSerThrTyrrhAlaAspAlaLeuTrpPglTyrrhIleTh 273
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Db 1029 CGAGTCAAGCGCGCTGAGTTCGCGAGCTACGCAAGATGCGCTGAGGGGGGTGTAC 1088
QY 273 rleuThrThrlleclYrrclYaspLysThrProleuThrTrpleuGlyArgleuLeuSe 293

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Db 1089 AGTCACCCACATCGGCTATGGGACAGAGTGGCCACAGCTGGGTGGGAGACCATTCGC 1148
QY 293 rAlaGlyPheAlaLeuLeuGlyIleSerPheAlaLeuProAlaGlyIleLeuGlySe 313
Db 1149 CTCCTGCTTCTCTCTTCCATCTCTCTTCTGCTCCACAGCGGGATTCCTGGCTC 1208
QY 313 rGlyPheAlaLeuValGlnGlnHisArgGlnHisPheGlnHisArgArgAs 333
Db 1209 GGGGTTTCCCTGAAGGTGCACACAGACAGAGCGAAGACACTTAACCGGACATCCC 1268
QY 333 nProAlaAlaAsnLeuIleGlnCysValTrpArgSerTyrrAlaAlaAspGlnLysSerVa 353
Db 1269 GCGCGACACCTCATCTACATTCAGACCGCATGAGTGTATGCTGCCAGAACCCCATCTC 1328
QY 353 lSerIleAlaThrTrpLysProHisLeuLysAlaLeu-----HisThr---CysSe 369
Db 1329 CTCCT-----ACCTGGAAGATCTACATCCGGAAGGCCCGCCGAGCCACACTTCGCTGC 1382
QY 369 rProThrAsnGlnLysLeuSerPheLysGlnArgValArgMetAlaSerProArgGlyG 389
Db 1383 ACCCAGCCCCCAACCC-----AAGAGCTCTGTGGTGGTAAGAAAAAAGTTCA 1433
QY 389 nSerIleLysSerArgGlnAlaSerValGlyAspArgArgSerProSerThrAspIleTh 409
Db 1434 GCTGGACAAAGACAATGGGTGATCTCTGAGAGAAAGATGCTACAGTCCCATATCAC 1493
QY 409 rAlaGlnGlySerProThrLysValGlnLysSerTrpSer-----PheAsnAspAr 426
Db 1494 GTGGACACCCCGAGAGAGCGGCGGTGACACACTTCTGTGCGAGCGGTGACAGTTCC 1553
QY 426 gThrArgPheArgProSerLeuArgLeuLysSerSerGlnProLysProValIleAspAl 446
Db 1554 TGTAAGAGAGAGCCCAACATG---CTGGAAGTGAAGCAATGCCCAT----- 1596
QY 446 aAspThrAlaLeuGlyThrAspAspValTyrrAspGlnLysGlnCysAspValSe 466
Db 1597 -----TTCATGGAAGACCAACAGCTTCGCCGAGAC-----CTGAGACTGGA 1637
QY 466 rValGluAspLeuThrProProLeu-----LysTh 476
Db 1638 AGGGAGACTGTGCTGACACCATATCCACATCTCCACAGCTGGCGGAACACCATCGGC 1697
QY 476 rValIleArgAlaIleArgIleMetLysPheHisValAlaLysArgLysPheLysGlnTh 496
Db 1698 CACCATTAAGTCAATTGACGACATGCACTTGTGGCCAGAGAAATTCACAGAAC 1757
QY 496 rLeuArgProTyrrAspValLysAspValIleGlnGlnTyrrSerAlaGlyHisLeuAspMe 516
Db 1758 GCGGAACCTTACATGTCGCGGACGATGACAGTACAGTGCAGAGGCCACCTCAACCT 1817
QY 516 tLeuGlyArgGlyLeuLysSerLeuGlnThrArgValAspGlnIleLeuGlyLysGln-- 535
Db 1818 CATGCTGCGCATCAAGAGCTGACAGAGAGGCTGAGACCATGTCATTGGGAACCCCTCACT 1877
QY 536 ----lLeThrSerAspLysLysSerArgLysIleThrAlaGlnHisGlnThThrAs 554
Db 1878 GTTCATCTCCCTCAGAAAGAGACAGATCGC-----GG 1913
QY 554 pAspLeuSerMetLeuGlyArgValValLysValGlnLysGlnValGlnSerIleGluSe 574
Db 1914 CAGCAACACGATCGCGCCCGCCGACAGGAGTAGAAGACAGAGTGCACGACCTGAGCCA 1973
QY 574 rLysLeuAspCysLeuLeuAspIleTyrrGlnGlnValLeuArgLysGlySer--AlaSerA 594
Db 1974 GAGGCTGCGCACTCTACCGACATGCTTCACACAGCTGCTCTCTTCGACACGGTGACAC 2033
QY 594 lAlaLeuAlaLeuAlaSerPheGlnIleProProPheGlnCysGlnGlnIleThrSerAspTyrg 614
Db 2034 CCGCGGACAGGCGGCGC-----CCCGCAGAGAGGCGGCGGCACATACCCAGCC 2084
QY 614 lnsrProValAspSer---LysAspLeuSerGlySer--AlaGlnAsnSerGlyCysLeu 632

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Db 2085 CTGGCGGACGAGTGGGAGCTCCGTGCACCCCTGAGCTCTTCTGCCACCAACACCCCTGCCAC 2144
QY 633 SerArgSerThrSer-----AlaAsnIleSerArgGlyLeu 644
Db 2145 CTACAGACAGCTGACCCGTGCCAGAGAGGCCCCCATGAGAGGCTCTGAGAGGGGAGATCG 2204
QY 645 GlnPheIleLeuThrProAsnGlnPheSerAlaGlnThrPhe-----TyrrAlaLeuSer 662
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QY 663 ProThrMetHis-----SerGlnAlaThrGlnValProIleSerGlnSerAspGly 679
Db 2265 GAAGGAGGCGCCCTCTTAAGAGCCCAAGAGAGAGAGAGAGCCCATCTTCAGAG----- 2315
QY 680 SerAlaValAlaAlaThrAsnThrIleAlaAsnGlnIleAsnThrAlaProLysProAla 699
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RESULT 15
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; Sequence 1, Application US/09597735
; Patent No. 6420124

GENERAL INFORMATION:
; APPLICANT: Keating, Mark T.
; APPLICANT: Sanguinetti, Michael C.
; APPLICANT: Curran, Mark E.
; APPLICANT: Landes, Gregory M.
; APPLICANT: Conners, Timothy D.
; APPLICANT: Burr, Timothy C.
; APPLICANT: Spiawski, Igor

TITLE OF INVENTION: KVIDT1 - A LONG QT SYNDROME GENE
; FILE REFERENCE: 2323-133
; CURRENT APPLICATION NUMBER: US/09/597,735
; CURRENT FILING DATE: 2000-06-19
; EARLIER APPLICATION NUMBER: 09/135,010
; EARLIER FILING DATE: 1998-08-17
; EARLIER APPLICATION NUMBER: 60/094,477
; EARLIER FILING DATE: 1998-07-29
; EARLIER APPLICATION NUMBER: 08/921,068
; EARLIER FILING DATE: 1997-08-29
; EARLIER APPLICATION NUMBER: 08/739,383
; EARLIER FILING DATE: 1996-10-29
; EARLIER APPLICATION NUMBER: 60/019,014
; EARLIER FILING DATE: 1995-12-22
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 1
; LENGTH: 3181
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (163)..(2190)

US-09-597-735-1

Alignment Scores:
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Score: 1116.50 Matches: 294
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GenCore version 5.1.3
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Run on: January 11, 2003, 18:00:47 ; Search time 82 Seconds
(Without alignments)
4765.997 Million cell updates/sec

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Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 389086 seqs, 220051671 residues

Total number of hits satisfying chosen parameters: 778172

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Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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Database : Published Applications_NA:

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	4547	100.0	2772	US-09-825-147-1	Sequence 1, Appl1
3	4547	100.0	3111	US-09-825-147-3	Sequence 3, Appl1
4	4527.5	99.6	2694	US-09-810-796-2	Sequence 2, Appl1

5	4523.5	99.5	3071	US-09-810-796-1	Sequence 1, Appl1
6	4513.5	99.3	3074	US-09-813-148-1	Sequence 1, Appl1
7	1792.5	39.4	3287	US-10-128-870-19	Sequence 19, Appl1
8	1790.5	39.4	2169	US-10-128-870-22	Sequence 22, Appl1
9	1587.5	34.9	2565	US-10-128-870-26	Sequence 26, Appl1
10	1207.5	26.6	900	US-10-128-870-5	Sequence 5, Appl1
11	1201.5	26.4	900	US-10-128-870-3	Sequence 3, Appl1
12	1114	24.5	2028	US-09-840-125-1	Sequence 1, Appl1
13	1094	24.1	2821	US-09-880-107-3358	Sequence 3358, Ap
14	1085	23.9	930	US-10-128-870-17	Sequence 17, Appl1
15	993.5	21.8	735	US-10-128-870-7	Sequence 7, Appl1
16	901.5	19.8	896	US-10-128-870-1	Sequence 1, Appl1
17	486.5	10.7	416	US-09-860-352-13343	Sequence 13343, A
18	290	6.4	429	US-09-783-590-4509	Sequence 4509, Ap
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20	260.5	5.7	1917	US-10-024-623-12	Sequence 12, Appl1
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23	243	5.3	2064	US-10-062-879-3	Sequence 3, Appl1
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32	217.5	4.8	2867	US-09-954-456-1227	Sequence 2354, Ap
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34	217	4.8	1599	US-09-993-811-4	Sequence 5, Appl1
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36	209	4.6	3473	US-09-993-811-5	Sequence 15, Appl1
37	209	4.6	3474	US-09-993-811-11	Sequence 15, Appl1
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39	192.5	4.2	1278	US-10-016-647-1	Sequence 1, Appl1
40	192.5	4.2	1844	US-10-016-647-3	Sequence 3, Appl1
41	180.5	4.0	1740	US-09-922-3644-15	Sequence 15, Appl1
42	180.5	4.0	1740	US-09-254-590-15	Sequence 15, Appl1
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44	178	3.9	1740	US-09-922-3644-21	Sequence 21, Appl1
45	178	3.9	1740	US-09-254-590-21	Sequence 21, Appl1

ALIGNMENTS

RESULT 1
US-09-810-796-3
; Sequence 3, Application US/09810796
; Patent No. US20020102677A1
; GENERAL INFORMATION:
; APPLICANT: Jega, Timothy James
; TITLE OF INVENTION: KCON5, a No. US20020102677A1 Potassium Channel
; FILE REFERENCE: 018512-005010US
; CURRENT APPLICATION NUMBER: US/09/810,796
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 60/190,954
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 2667
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human outwardly rectifying, voltage-gated
; OTHER INFORMATION: potassium channel KCON5-2 coding sequence
; NAME/KEY: CDS
; LOCATION: (1)..(2667)
; OTHER INFORMATION: KCON5-2
US-09-810-796-3

Alignment Scores:

Pred. No.: 0
 Score: 4547.00
 Percent Similarity: 100.00%
 Best Local Similarity: 100.00%
 Query Match: 100.00%
 DB: 10
 Gaps: 0

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; Patent No. US20020042505A1
; GENERAL INFORMATION:
; APPLICANT: Hu, Yi
; APPLICANT: Kieke, James Alvin
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael C.
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. us20020042505A1el Human Ion Channel Protein and
; FILE REFERENCE: LEX-0160-USA
; CURRENT APPLICATION NUMBER: US/09/825,147
; PRIOR APPLICATION NUMBER: 2001-04-03
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2772
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-825-147-1
Alignment Scores:
Pred. No.: 0 Length: 2772
Score: 4547.00 Matches: 888

Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Gaps: 0
DB: 10
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Db 106 ATGAGAGATGTGGAGTGGCGCGGAGGAGGTGCTGTAAGTCCGCGCAGCCAGGGGC 165
QY 21 AspGlyLeuLeuLeuLeuGlyThrArgAlaAlaThrLeuGlyGlyGlyGlyGlyLeu 40
Db 166 GACGGCGCTGTACTGCTGGGACCGCGCGCGCCACGCTGGCGGGGGGTGGCCTG 225
QY 41 ArgGlySerArgArgGlyLysGlnGlyAlaArgMetSerLeuLeuGlyLysProLeuSer 60
Db 226 AGGAGAGCGCGCGGCAAGCAGGGGGCCCGATGAGCCGTGGGGAACCGCTCTCT 285
QY 61 TyrThrSerSerGlnSerCysArgArgAsnValLysTyrArgArgValGlnAsnTyrLeu 80
Db 286 TACACGATAGCCAGAGCTCCCGCGCACGTCAAGTACCGCGCGGTGCAGAACTACCTG 345
QY 81 TyrAsnValLeuGluArgProArgGlyTyrAlaPheIleTyrHisAlaPheValPheLeu 100
Db 346 TACACGCTGTGAGAGAGACCCCGCGGCTTCACTACACACGCTTCGTTTCTC 405
QY 101 LeuValPheGlyLysLeuIleLeuSerValPheSerThrIleProGluHisTyrLysLeu 120
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QY 121 AlaSerSerCysLeuLeuIleLeuGluPheValMetIleValIlePheGlyLeuGluPhe 140
Db 466 GCCTCAAGTTGGCTCTTGATCTCGAGTTGCTGATGATGCTGCTTGTGGTGGAGTTC 525
QY 141 IleIleArgIleTyrPheSerAlaGlyCysCysArgTyrArgGlyTyrGlnGlyArgLeu 160
Db 526 ATCATTCGAATCTGCTGCGGGTGGCTGTGCTGATATAGAGATGAGCAAGAACTG 585
QY 161 ArgPheAlaArgLysProPheCysValIleAspThrIleValIleAlaSerIleAla 180
Db 586 AGGTGTGCTCGAAAGCCCTGCTGTATAGATACCATTTCTTATCCGCTTCAATGACA 645
QY 181 ValValSerAlaLysThrGlnGlyAsnIlePheAlaThrSerAlaLeuArgSerLeuArg 200
Db 646 GTTGTTCGCAAAACTCAGGTAATATTTTGGCAGCTGTGCACTCAGAACTCTCCGT 705
QY 201 PheLeuGlnIleLeuArgMetValArgMetAspArgArgGlyThrTyrLysLeuLeu 220
Db 706 TTCCTACAGATCTCCGATGGTGGCATGACCGAAGGGAGGCACTTGGAAATTACTG 765
QY 221 GlySerValValTyrAlaHisSerLysGluLeuIleThrAlaTyrPyrIleGlyPheLeu 240
Db 766 GGTTCAGTGGTTATATCTCAGCAGCAAGAAATTAATCACACTTGGTACATAGGATTTTGG 825
QY 241 ValLeuIlePheSerSerPheLeuValTyrLeuValGluLysAspAlaAsnLysGluPhe 260
Db 826 GTTCTTATTTTTCGCTTCCCTTGTCTATCTGCTGGAAAGAGATGCCAATAAGACTTT 885
QY 261 SerThrTyrAlaAspAlaLeuTyrTrpGlyThrIleThrLeuThrThrIleGlyTyrGly 280
Db 886 TCTACATATGACAGATCTCTGCTGGGGCACAAATTAATCACTGCAACTATTTGGCTATGCA 945
QY 281 AspLysThrProLeuThrTrpLeuGlyArgLeuLeuSerAlaGlyPheAlaLeuLeuGly 300
Db 946 GACAAAGCTCCCTAACTTGGCTGGGAGAACTTCTTTGACAGCCTTTGGACTCTTGGC 1005
QY 301 IleSerPhePheAlaLeuProAlaGlyIleLeuGlySerGlyPheAlaLeuLysValGln 320
Db 1006 ATTTCTTCTTTCACACTTCCCGCGCATTTCTTGCTCAGGTTTGCATTAATAAGTACAA 1065
QY 321 GluGlnHisArgGlnLysHisPheGlyLysArgArgAsnProAlaAlaAsnLeuIleGln 340

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Db 1066 GAACACACCGCCGAAACACCTTTGAGAAAAGAGAAACCCAGCTCCACCTCATTCAG 1125
QY 341 CysValThrPArgSerThrAlaAlaAspGluIleuSerValSerIleAlaThrTrpIysPro 360
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Db 1126 TGTGTTGGGCTACTTACGACGCTGATGAGAAATCTGTTCCATTGCAACCTCGAAGCCA 1185
QY 361 HisLeuLysAlaLeuHisThrCysSerProThrAsnGlnIleuSerPheLysGluArg 380
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Db 1186 CACTTGAAGGCTTGACACCTGACCCCTACCAATCAGAACCTTAAGTTTAAGAGCGCA 1245
QY 381 ValArgMetAlaSerProArgGluInserIleLysSerArgAlaSerValGlyAsp 400
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Db 1246 GTGGCGCATGGCTACGCCAGGGCCAGAGTATTAAAGCCGCAAGCCCTCATAGGTGAC 1305
QY 401 ArgArgSerProSerThrAspIleThrAlaGluIleuSerProThrLysValGlnLysSer 420
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Db 1306 AGGAGTCCCAACACGACGACATCACCCGAGGCGACGCCCAAAATGTCAGAGAC 1365
QY 421 TrpSerPheAsnAspArgThrArgPheArgProSerLeuArgLeuLysSerGlnPro 440
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Db 1366 TGGAGCTTCAACGACCGACCCGCTTCGGCCCTGCTGCTGCTGCTGCTGCTGCTGCTG 1425
QY 441 LysProValIleAspAlaAspThrAlaLeuGluIleThrAspAspValIleAspGluIle 460
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Db 1426 AAACACAGATAGATGCTGACACACACCCCTTGGCAGTATGATGATGATGATGATGATG 1485
QY 461 CysGlnCysAspValSerValGluAspLeuThrProProLeuLysThrValIleArgAla 480
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QY 481 IleArgIleMetLysPheHisValAlaLysArgLysPheLysGluIleThrLeuArgProTrp 500
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Db 1546 ATCGAATATTGAAATTTCAATGTTGCAAAACGAAAGTTTAAAGAAACATTACCTCATAT 1605
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Db 1606 GATGTAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1665
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QY 581 AspiLeuArgGlnValLeuArgLysGlySerAlaSerAlaLeuAlaLeuAlaSerPhe 600
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Db 1846 GACATCTTCAACAGGCTCTTGGAAAGGCTCTGCTCAGCCCTTGGCTTGGCTTCAATTC 1905
QY 601 GlnIleProProPheGluLysGlnIleThrSerAspTrpGlnSerProValAspSerLys 620
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Db 1906 CAGATCCCAACCTTTGAATGATGACAGACATCTGACTATCAAAAGCCCTGAGATAGAAA 1965
QY 621 AspiLeuSerGlySerAlaGlnAsnSerGlyCysLeuSerArgSerThrSerAlaAsnIle 640
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Db 1966 GATCTTTCGGGCTTCGACACAAACAGTGGCTGCTTATCCAGATCAACCTACTGCAACATC 2025
QY 641 SerArgGlyLeuGlnPheIleLeuThrProAsnGluPheSerAlaGlnIleThrPheTrpAla 660
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Db 2026 TCGAAGAGCTGACGATCTTCTGACGCAAAAGAGTTCAAGTCCCAAGACTTTCTACGGC 2085
QY 661 LeuSerProThrMetHisSerGlnAlaThrGlnValProIleSerGlnSerAspGlySer 680
   |||||
Db 2086 CTTACCCCTACTATGACAGTCAAGACACACAGTGCCTCAATTGTCAAAACGATGGCTCA 2145
QY 681 AlaValAlaAlaThrAsnThrIleAlaAsnGlnIleAsnThrAlaProLysProAlaAla 700
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Db 2146 GCAGTGGCAGCCACCAACCATTTGCAAAACCAAAATAATTCGCGCACCCAGCCAGCAGCC 2205

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Db 2266 ACTCTGACCCCTTAACTCTGACAGCTTACAGAAAGCATTTCTGTGACGTCACCACTGCTT 2325
QY 741 ValAlaSerLysGluAsnValGlnValAlaGlnSerAsnLeuThrLysAspArgSerMet 760
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QY 761 ArgLysSerPheAspMetGlyGlyGluThrLeuLeuSerValCysProMetValProLys 780
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QY 781 AspiLeuGlyLysSerLeuSerValGlnAsnLeuIleArgSerThrGluLeuAsnIle 800
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RESULT 3
US-09-825-147-3
; Sequence 3, Application US/09825147
; Patent No. US20020042505A1
; GENERAL INFORMATION:
; APPLICANT: Hu, Yi
; APPLICANT: Kieke, James Alvin
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael C.
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OR INVENTION: No. US20020042505A1el Human Ion Channel Protein and
; TITLE OF INVENTION: Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0160-USA
; CURRENT APPLICATION NUMBER: US/09/825,147
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/194,255
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 3111
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-825-147-3

Alignment Scores:
Pred. No.: 0 Length: 3111
Score: 4547.00 Matches: 888
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0

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Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0
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DB 225 GAGGGCTGTACTGCTGGGACCCGCGGCCACGCTGGTGGCGGGGCGGGCTG 284
QY 41 ArgGluSerArgArgGlyLysGlnGlyAlaArgMetSerLeuLeuGlyLysProLeuSer 60
DB 285 AGGAGACAGCCGCGGGGCAAGAGGGGGCCCGGATGAGCCCTGCTGGGAACCCGCTCTCT 344
QY 61 TyrThrSerSerGlnSerCysArgArgAsnValLysTyrArgArgValGluAsnTyrLeu 80
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QY 81 TyrAsnValLeuGluArgProArgGlyTyrAlaPheLeuIleTyrHisAlaPheValPheLeu 100
DB 405 TACAAAGTGTGAGAGAACCCCGCGCTGGGCTTGCATCACTACACGCTTGGTTTCTC 464
QY 101 LeuValPheGlyCysLeuLeuLeuSerValPheSerThrIleProGlnHisThrLysLeu 120
DB 465 CTGCTCTGGTGGTTCGTTGATTTGTCACTGCTTTCTACCATCCCTGAGCACACAATTTG 524
QY 121 AlaSerSerCysLeuLeuLeuLeuGluPheValMetIleValValPheGlyLeuGluPhe 140
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DB 1305 GTGCGATGGCTAGCCCGAGGGGCCAGAGTATTAAAGCCGCAAGGCTCAGTAGGTGAC 1364
QY 401 ArgArgSerProSerThrAspIleThrAlaGlyLysProThrLysValGlnLysSer 420
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QY 421 TrpSerPheAsnAspArgThrArgPheArgProSerLeuArgLeuLysSerSerGlnPro 440
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QY 441 LysProValIleAspAlaAspThrAlaLeuGlyThrAspAspValTyrAspGluLysGly 460
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QY 581 AspIleTyrGlnGlnValLeuArgLysGlySerAlaSerAlaLeuAlaLeuAlaSerPhe 600
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QY 601 GlnIleProProPheGluCysGlnGlnThrSerAspTyrGlnSerProValAspSerLys 620
DB 1965 CAGATCCCACTTTTGAATGTGAACAGACATCTGACTATCAAGCCCTGTGGATAGCAAA 2024
QY 621 AspLeuSerGlySerAlaGlnAsnSerGlyCysLeuSerArgSerThrSerAlaAsnIle 640
DB 2025 GATCTTTCGGTTCCGACAAAACAGTGGCTGCTTATCCAGATCAACTATGTCACCAATC 2084
QY 641 SerArgGlyLeuGlnPheIleLeuThrProAsnGluPheSerAlaGlnIleThrPheTyrAla 660
DB 2085 TCGAGAGGCTCGACAGTTCAATTGACGCCCAATGACGTTCAGTCCCGACACTTTCACGGC 2144
QY 661 LeuSerProThrMetHisSerGlnAlaThrGlnValProIleSerGlnSerAspGlySer 680
DB 2145 CTTAGCCCTACTATGACAGCTCAAGCAACACAGTGCATATGTGTAAGCGATGGCTCA 2204
QY 681 AlaValAlaAlaThrAsnThrIleAlaAsnGlnIleAspThrIleArgProLysProAlaAla 700
DB 2205 GCAGTGGCAGCCACCAACCATTCGCAAAACCAATAAATAGGACCCCAAGCCAGCAGCC 2264
QY 701 ProThrThrLeuGlnIleProProProLeuProAlaIleLysHisLeuProArgProGln 720

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Db 2325 ACTCTGCACCTTACACCTTGACAGGCTTACAGAAAGCATTTCTGACGTCACACCTGCTT 2384
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QY 761 ArgLysSerPheAspMetGlyGlyGluThrLeuLeuSerValCysPrometValProLys 780
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QY 801 GlnLeuSerGlySerGluSerSerGlySerArgGlySerGlnAspPheLysProLysTrp 820
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QY 861 ThrGluArgSerArgSerSerGlnSerIleCysLysAlaGlyGlnSerThrAspAlaLeu 880
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Db 2805 AGCTTGCTCATGTCAAACTGAAA 2828

RESULT 4
US-09-810-796-2
; Sequence 2, Application US/09810796
; Patent No. US20020102677A1
; GENERAL INFORMATION:
; APPLICANT: Jeda, Timothy James
; TITLE OF INVENTION: KCON5, a No. US20020102677A1e1 Potassium Channel
; FILE REFERENCE: 018512-005010US
; CURRENT APPLICATION NUMBER: US/09/810,796
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 60/190,954
; PRIOR FILING DATE: 2000-03-21
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 2694
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human outwardly-rectifying, voltage-gated
; OTHER INFORMATION: potassium channel KCON5-1 coding sequence
; NAME/KEY: CDS
; LOCATION: (1)-(2694)
; OTHER INFORMATION: KCON5-1
US-09-810-796-2

Alignment Scores:
Pred. No.: 0 Length: 2694
Score: 4527.50 Matches: 887
Percent Similarity: 99.00% Conservative: 1
Best Local Similarity: 98.89% Mismatches: 0
Query Match: 99.57% Indels: 9
DB: 10 Gaps: 1

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Db 61 GAGGGCTGCTACTGCTGGGACCCCGCGGCCAGCTTGGTGGCGGCGGCGGCTGCTG 120
QY 41 ArgGluSerArgArgGlyLysGlnGlyAlaArgMetSerLeuLeuGlyLysProLeuSer 60
Db 121 AGGGAAGCGCGCGGCGGAGAGAGGCGCGCGGATGAGCTGCTGAGGAGAGCGGCTCT 180
QY 61 TyrThrSerSerLysSerCysArgArgAsnValLysTyrArgArgValGlnAsnTyrLeu 80
Db 181 TACACAGATAGCCAGAGCTCCGCGGCAAGTCAAGTACCGCGGCTGACAGAACTACCTG 240
QY 81 TyrAsnValLeuGlnLysArgProArgGlyTyrAlaPheIleTyrHisAlaPheValPheLeu 100
Db 241 TACAACTGCTGGAGAGAGACCCCGGCTGGGCTTCATCTACACAGCTTGGTTTCTC 300
QY 101 LeuValPheGlyCysLeuIleLeuSerValPheSerThrIleProGlnHisThrLysLeu 120
Db 301 CTGCTCTTGGTTCCTGATTTGTGAGTGTCTACACATCCCTGAGCACACAAATTTG 360
QY 121 AlaSerSerCysLeuLeuIleLeuGluPheValMetIleValPheGlyLeuGluPhe 140
Db 361 GCCTCAAGTTCCTCTTGATCCCTGGAGCTGTGTGATGTCGTCCTTGGTTGGAGTTTC 420
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QY 161 ArgPheAlaArgLysProPheCysValIleAspThrIleValLeuIleAlaSerIleAla 180
Db 481 AGGTTGCTCGAAGAGCCCTTCTGTATAGATACCATTTGTTCTATGCTTCATAGACA 540
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Db 541 GTTGTTTCGCAAAACCTCAGGGTAATATTTTCCACGCTGACACAGAGTCCGT 600
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Db 601 TTCCTACAGATCTCCGCGATGTCGTCATGACCGGAGGAGGACCTTGCATAATTACTG 660
QY 221 GlySerValValTyrAlaHisSerLysGluLeuIleThrAlaTyrTyrIleGlyPheLeu 240
Db 661 GGTTCAGTGGTTATGCTCAGACAGCAAGAAATTAATCACAGCTTGGTACATFAGATTG 720
QY 241 ValLeuIlePheSerSerPheLeuValTyrLeuValGlyLysAspAlaAsnLysGluPhe 260
Db 721 GTTCTATATTTTTCGTTCTTCCTGCTATCTGTGTGAAAGGATGCAATAAAGTTT 780
QY 261 SerThrTyrAlaAspAlaLeuTyrTyrGlyThrIleThrLeuThrThrIleGlyTyrGly 280
Db 781 TCTACATATGACATGCTCTCTGTCGTCGACAAATTACATTGACACACTATTTGGCTATGCA 840
QY 281 AspLysThrProLeuThrTyrLeuGlyArgLeuLeuSerAlaGlyPheAlaLeuLeuGly 300
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QY 321 GluGlnHisArgGlnLysHisPheGluLysArgArgAsnProAlaAlaAsnLeuIleGln 340
Db 961 GAACCAACCGCCAGAGAACTTTGAGAAAAGAAAGAACCCAGCTGCCAACTCATTCAG 1020
QY 341 CysValTyrArgSerTyrAlaAlaAspGluLysSerValSerIleValThrTyrLysPro 360

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 QY 372 AaG1LysLeuSerPheYsGluArgValArgMetAlaSerProArgGlyGlnSerIle 391
 Db 1141 AGTCACAAGCTAGTTTAAAGAGCAGAGTGCATGGCTACGCCAGGCGCCAGAGTATT 1200
 QY 392 LysSerArgGlnAlaSerValGlyAspArgArgSerProSerThrAspIleThrAlaGlu 411
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 RESULT 5
 US-09-810-796-1
 ? Sequence 1, Application US/09810796
 ? Patent NO. US20020102677A1
 ? GENERAL INFORMATION:
 ? APPLICANT: Jeda, Timothy James
 ? TITLE OF INVENTION: KCNO5, a No. US20020102677A1 Potassium Channel
 ? FILE REFERENCE: 018512-005010US
 ? CURRENT APPLICATION NUMBER: US/09/810, 796
 ? PRIOR FILING DATE: 2001-10-12
 ? PRIOR APPLICATION NUMBER: US 60/190, 954
 ? NUMBER OF SEQ ID NOS: 17
 ? SOFTWARE: PatentIn Ver. 2.1
 ? SEQ ID NO 1
 ? LENGTH: 3071
 ? TYPE: DNA
 ? ORGANISM: Homo sapiens
 ? FEATURE:
 ? OTHER INFORMATION: human outwardly rectifying, voltage-gated
 ? NAME/KEY: CDS
 ? LOCATION: (10)..(2703)
 ? OTHER INFORMATION: KCNO5-1
 US-09-810-796-1
 Alignment Scores:
 Pred. No.: 0 Length: 3071
 Score: 4523.50 Matches: 886
 Percent Similarity: 98.89% Conservative: 1
 Best Local Similarity: 98.77% Mismatches: 1
 Query Match: 99.48% Indels: 9
 DB: 10 Gaps: 1
 US-09-810-796-5 (1-888) x US-09-810-796-1 (1-3071)

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RESULT 6
US-09-813-148-1
Sequence 1, Application US/09813148
Patent No. US20020076809A1
GENERAL INFORMATION:
APPLICANT: STEINMEYER, Klaus
APPLICANT: LERCHE, Christian
APPLICANT: SCHERER, Constanze
APPLICANT: SEBOHM, Guisard
APPLICANT: BUSCH, Andreas E.
TITLE OF INVENTION: POTASSIUM CHANNEL PROTEIN KCNO5, A NEW TARGET FOR DISEASES OF CEN
TITLE OF INVENTION: NERVOUS SYSTEM AND CARDIOVASCULAR SYSTEM
FILE REFERENCE: 38005-119
CURRENT APPLICATION NUMBER: US/09/813,148
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: DE 100 13 732.6
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: US 60/194,041
PRIOR FILING DATE: 2000-04-03
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1
LENGTH: 3074
TYPE: DNA
ORGANISM: Homo sapiens
US-09-813-148-1

Alignment Scores:
Pred. No.: 0 Length: 3074
Score: 4513.50 Matches: 885
Percent Similarity: 98.77% Conservative: 1
Best Local Similarity: 98.66% Mismatches: 2
Query Match: 99.26% Indels: 9
DB: 10 Gaps: 1

US-09-810-796-5 (1-888) x US-09-813-148-1 (1-3074)
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 Db 1895 ACCACAGACATCTCATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1954
 QY 572 IleGlnSerLysLeuAspCysLeuLeuAspIleTyrGlnGlnValLeuArgLysGlySer 591
 Db 1955 ATGGAATCCAGAGCTGGAGCTGCTTACTAGACATCTATCAACAGGCTCTTCGGAAGAGCT 2014
 QY 592 AlaSerAlaLeuAlaLeuAlaSerPheGlnIleProProPheGlnCysGlnGlnThrSer 611
 Db 2015 GCGTCAGCCCTCGCTTGGCTTCAATCCAGATCCACCTTTGATGATGATGATGATGAT 2074
 QY 612 AspTyrGlnSerProValAspSerLysAspLeuSerGlySerAlaGlnAsnSerGlyCys 631
 Db 2075 GACTATCTAAAGCCCTGGAGTAGCAAAAGATCTTTCGGGTCCGCAAAACAGTGGCTGC 2134
 QY 632 LeuSerArgSerThrSerAlaAsnIleSerArgLysLeuGlnPheIleLeuThrProAsn 651
 Db 2135 TTATCCAGATCACTAGTGCACATCTCGAAGGCTCGAGTTGATCTGACGCCCAAT 2194
 QY 652 GluPheSerAlaGlnThrPheTyrAlaLeuSerProThrMetHisSerGlnAlaThrGln 671
 Db 2195 GAGTTTCAGTGCAGACTTCTTACGCGCTTACGCCCTTACTATGACACAGTCAACACACAG 2254
 QY 672 ValProLysSerGlnSerAspGlySerAlaValAlaIleThrAsnThrIleAlaAsnGln 691
 Db 2255 GTGGCAATTATCTCAAAAGGATGGCTCAGAGTGGCAGCCACCAACACCTTGGCAAAACCA 2314
 QY 692 IleAsnThrAlaProLysProAlaIleAlaIleProThrLeuGlnIleProProLeuPro 711
 Db 2315 ATAATATGAGGACCAACCAACGACGCCCAACTTTTACAGATCCACCTCTCTCCCA 2374
 QY 712 AlaIleLysHISLeuProArgProGlnThrLeuHISProAsnProAlaGlyLeuGlnGlu 731
 Db 2375 GCCATCAAGCATCTGGCCAGGCGCAAAACTCTGCAACCCCTGACAGGCTTACAGGAA 2434

QY 732 SerIleSerAspValThrThrCysLeuValAlaSerLysGlnAsnValGlnValAlaGln 751
 Db 2435 AGCATTTCTGACGTCACACCTGCTTGTTCCTTCCAAAGAAATGTCAGGTGCACAG 2494
 QY 752 SerAsnLeuThrLysAspArgSerMetArgLysSerPheAspMetGlyGlyGlnThrLeu 771
 Db 2495 TCAATCTCACCAAGACCGTTCTTATGAGGAAACCTTTGACATGGAGGAAACCTCTG 2554
 QY 772 LeuSerValCysPrometValProLysAspLeuGlyLysSerLeuSerValGlnAsnLeu 791
 Db 2555 TTGCTGTCTGCTGCCATGCTGTGCGCAAGACTTGGCAATCTTTGCTGTGCAAAACCTG 2614
 QY 792 IleArgSerThrGlnIleLeuAsnIleGlnLeuSerGlySerGlnSerSerGlySerArg 811
 Db 2615 ATCAGTGTGACCGAGGAAGTGAATATACACTTTCAGGAGTCAAGTCAAGTGGCTCCAA 2674
 QY 812 GlySerGlnAspPheTyrProLysTrpArgGlnSerLysLeuPheIleThrAspGlnGlu 831
 Db 2675 GGCACCCAAAGATTTTACCCTCAATGGAGGAATCCAAATTTGTTTAACTGATGAAGAG 2734
 QY 832 ValGlyProGlnGlnThrGlnThrAspThrPheAspAlaIleProGlnProAlaArgGlu 851
 Db 2735 GTGGCTCCCGAAGAGACAGACAGACACTTTGATGATGATGATGATGATGATGATGAT 2794
 QY 852 AlaAlaPheAlaSerAspSerLeuArgThrGlyArgSerArgSerSerGlnSerIleCys 871
 Db 2795 GCTGCTTGTGCTACAGACTCTTAAGAGACTGAGAGTCAACAGATCACTGAGACATTTG 2854
 QY 872 LysAlaGlyGlnSerThrAspAlaLeuSerLeuProHisValLysLeuLys 888
 Db 2855 AAGCGAGGAGAAAGTACAGATGCTCCAGCTTGCCTCATGATGCAAACTGAA 2905

RESULT 7

US-10-128-870-19

; Sequence 19, Application US/10128870
 ; Patent No. US20020168724A1

GENERAL INFORMATION:

; APPLICANT: Bliant, Michael A.
 ; APPLICANT: Dworetzky, Steven
 ; APPLICANT: Gridkoff, Valentin K.
 ; APPLICANT: Levesque, Paul C.
 ; APPLICANT: Little, Wayne A.
 ; APPLICANT: Neubauer, Michael G.
 ; APPLICANT: Yang, Wen-Pin
 ; TITLE OF INVENTION: KCNO POTASSIUM CHANNELS AND METHODS OF MODULATING SAME
 ; FILE REFERENCE: DC58adiV
 ; CURRENT APPLICATION NUMBER: US/10/128, 870
 ; PRIOR FILING DATE: 2002-04-24
 ; PRIOR APPLICATION NUMBER: 09/105,058
 ; PRIOR FILING DATE: June 26, 1998
 ; PRIOR APPLICATION NUMBER: 60/055,599
 ; PRIOR FILING DATE: August 12, 1997
 ; NUMBER OF SEQ ID NOS: 28
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 19
 ; LENGTH: 3287
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-128-870-19

Alignment Scores:

Pred. No.: 1,02e-167 Length: 3287
 Score: 1792.50 Matches: 411
 Percent Similarity: 58.908 Conservative: 102
 Best Local Similarity: 47.198 Mismatches: 181
 Query Match: 39.428 Indels: 178
 DB: Gaps: 22

US-09-810-796-5 (1-888) x US-10-128-870-19 (1-3287)

QY 17 AlaIleArgLysAspGlyLeuLeuLeuGlnThrArgAlaIleThrLeuGlyGlyGly 36
 : : : ||| ||||| : : : |||

Db	160	TCACACCCGGAGGGGGCGCTGCTGATCCGCGGCTCCGAGGCCCCCAAG-----CGC	210
OY	37	GLYGLYGLYLEuArgGLuSerIArgAGLYLysGLINGLYAlaArgMetSerLeuLeuGLY	56
Db	211	GCGACGACTCTCAGCAACCTTCGCGGGCGGGCGCGCGCGCC-----GGG	255
OY	57	LysProLeuSerTyrThrSerSerGlnSerCysArgArgAsnValLysIArgAlaGVal	76
Db	256	AAGCCC-----CCCAAGCGCAAGCCCTTCTACCGCAAGCTG	291
OY	77	GLuAsnLYrLeuTYrAsnValLeuGLuArgProArgLYrPALaPheLeTYrHisAla	96
Db	292	CAGAAATTCCCTCTACAAACGTCGTGAGCGGGCGCGCGGTGGCGTTCATCTACACCGC	351
OY	97	PheValPheLeuLeuValPheGLYcysLeuILEuSerValPheSerThrIleProGLu	116
Db	352	TACGTCCTCCCTCGGTGTTTCTCTGCTGCTCGCTGCTGTCTGTCTTCCACCCATCAAGAG	411
OY	117	HisThrLysLeuAlaSerSerCysLeuLeuILEuGLuPheValMetIleValPhe	136
Db	412	TATGAGAAGACTCGAGCGGGCGCCCTACATCCTGGAATCGTACATCTGCTGTTT	471
OY	137	GLYLeuGLuPheIleIleArgIleIleTyrSerIleAGLYcysCysArgTYrArgLYr	156
Db	472	GCGCTGGAGTACTTCGTGCGGATGTGGGCCACAGCTCTGCTGCTGCTGCTGCTG	531
OY	157	GLuGLYArgLeuArgPheAlaArgLYsProPheCysValIleAspThrIleValLeuIle	176
Db	532	AGGGGCGCGCTCAAGTTGCCCGGGAACCGTTCTGTGTGATTTGACATCATGTGCTCATC	591
OY	177	AlaSerIleAlaValAlaSerAlaLYsThrGlnLYsIlePheAlaThrSerAlaLeu	196
Db	592	GCTCATTCGCGGTGGCGGGCGCGCTCCAGGGAACGTTTGGCACATCGCTGCTC	651
OY	197	ArgSerLeuArgPheLeuGlnIleLeuArgMetValArgMetAspArgArgLYGLYr	216
Db	652	CGAGCGCTGCGCTTCGTGAGATTCTCGGATGATCCGATGGACCGGGGGAGGACCC	711
OY	217	TrpLYsLeuLeuGLYSerValValTYrAlaHisSerLYsGLuLeuIleThrAlaTrpTYr	236
Db	712	TGGAACTGCTGGGCTGTGCTGTATGCCACAGCAAGGAGCGTGCTACCTGCTGGTAC	771
OY	237	IleGLYrPheLeuValLeuIlePheSerSerPheLeuValTYrLeuValGLYAspAla	256
Db	772	ATGCGCTCTCTTGTCTCATCCGCGCTCGTTCTGCTGATCTGGCAGCAAGAGGGGAG	831
OY	257	AsnLYsGLuPheSerThrTYrAlaAspAlaLeuTrpTrpLYrThrIleThrLeuThrThr	276
Db	832	AACGACACTTGTACACCTACCGCGGATGACCTGTGGTGGCGGATGCACGTGACACC	891
OY	277	IleGLYrGLYAspLYsThrPheLeuThrTrpLeuGLYrArgLeuLeuSerAlaGLYrPhe	296
Db	892	ATTGGTACGGGGACAGTACACCCCGACAGCTGGAGCGGAGGCTCTTGGGCAACCTTC	951
OY	297	AlaLeuLeuGLYrIleSerPhePheAlaLeuProAlaGLYrIleLeuGLYrSerGLYrPheAla	316
Db	952	ACCCATCATCGGTGTCTCTTCTTCGGGTGCGTGCAGGATCTTGGGGTGGTTGGC	1011
OY	317	LeuLYsValGLuGLuGlnHisArgGlnLYsHisPheGLYcysArgArgAsnProAlaIle	336
Db	1012	CTGAGAGCTTCAGAGCAGCAGCACAGGCAAGGCAACTTTGAAAGAGCGCGAACC	1071
OY	337	AsnLeuIleGlnCysValTYrPArgSerTYrAlaIleAsp-----	349
Db	1072	GCGCTGATCCAGTCCGGCTGGAGATTTCAGCCACCAACCTCTCGGGCACAGACCTGCAC	1131
OY	350	-----GLuLYsSerValSerIleAlaThrTrpLYs-----	359
Db	1132	TCCACGTGGCAGTACTACGAGCGGAACGGCTACCGCCATGTACAGTTGCAAACTCAA	1191
OY	360	-----ProHisLeuLYsAlaIleHisThr-----	367
Db	1192	ACCTACGGGGCTCCAGACTTATCCCGCGGTGAAACACAGCTGGAGCTGTGAGAAACCTTC	1251

OY	367	-----	367
Db	1252	AAGAGTAAATCTGGAGCTCGCTTTTCAGGAAGGAGACCCCGCCGAGCGCTGTCCAAAGTAA	133
OY	368	-----CysSerPro-----ThrAngInLysLeu	375
Db	1312	GGCAGCCCGCTGCAGAGAGGCCCTGTGTGATGCTGCCCGGACCGCTCTTACCCAGAAAGTCC	137
OY	376	SerPheLysGlnArgValArgMetaLaserProArgGlyInSerIleLysSerArgGln	395
Db	1372	AGTTTGAAAGATCGTGTC---TTCTCCAGCCCGGAGCGGTGCTGCCAAGGGAAGGCG	142
OY	396	AlaSerValGlyLasp-----ArgArgSerProSerThrAspIleThrAlaGlyLysSer	413
Db	1429	TCGCCCGCAGGCCCAACTGTGAGGGGGTACCACGCGCCAGCCAGCGCTCCAGGAGAGC	148
OY	414	ProThrLysValGlnLysSerTrpSerPheAsnAspArgThrArgPheArgProSerLeu	433
Db	1489	CCGAGCAGAGCTGCCCAAGAGGTGGAGCTTCGGGAGCCGACCGCGGCACGCCAGCTTTC	154
OY	434	ArgLeuLysSerSerGlnProLysProValIleAspAlaAspThrAlaLeuGlyThrAsp	453
Db	1549	CGCATCAAGGCTCGCGCGCTCACAGCGAG-----AACTCAGAAAGCAAGCTCCCGCGAGAG	160
OY	454	AspValTyrAspGlnLysGlyCysGlnCysAspValSerValGlnLysLeuThrProPro	473
Db	1603	GACATTTGGATGACAAAGAGCTGCCCGCTTCGAGTTTGACCCGAGACCTTGACCCCGGC	166
OY	474	LeuLysThrValIleArgAlaIleArgIleMetLysPheHisValAlaLysArgLysPhe	493
Db	1663	CTCAAAAGTCAGCATCAGAGACCGGTGTGTCTGATCGCGTCTGTGTCTCCAAAGCGGAATTTC	172
OY	494	LysGlnThrLeuArgProTyrAspValLysAspValIleGlnGlnLysSerAlaGlyHis	513
Db	1723	AAGAGAGAGCTCGCGGCTTACGAGCTGATGACAGCTCATCGAGCACTACCTACCCGCGCAC	178
OY	514	LeuAspMetLeuLysArgIleLysSerLeuGlnThrArgValLaspGlnIleLeuGlyLys	533
Db	1783	CTGGACATGCTGTCCGAAATTAAAGACCTCCGATCCAGAGTGAGGACCATGCTGGGGCGG	184
OY	534	GlyGlnIleThrSerAspLysLysSerArgLysLysIleThrAlaGlnHisGlnThrThr	553
Db	1843	GGCCACAGCATCACAGGAC---AAGAGCCGACACCAGAGGCCCGCGCCGAGGGGACTGCC	189
OY	554	AspAspLysSerMetLeuGlyArgValValLysValGlnLysGlnValGlnSerIleGln	573
Db	1900	GAGGAGCCCGCATGATGATGAGGACCGGCTCGGGAAGGTGGAGACGAGGTCTTGCCATGGAG	195
OY	574	SerLysLeuAspLysLeuLeuAspIleTyrGlnGlnValLeuArgLysGlySerAlaSer	593
Db	1960	AAGAACTGGACTTCCGTGGTGAATATTTACATCGAG-----CGATGTGC-----	2004
OY	594	AlaLeuAlaLeuAlaSerPheGlnIleProPheGlyLys	607
Db	2005	-----ATCCCCCGCAGACAGACCGAGGCTACTTTGGGGCC	2040
OY	608	-----GlnGlnThrSerAspTyrGlnSerProValLaspSerLysAspLeuSerLys	624
Db	2041	AAAGAGCCGAGAGCGCGCCCGCTGATCCACAGCCCGGAAACACCCCGGAG-----	2091
OY	625	SerAlaGlnAsnSerGlyCysLeuSerArgSerThrSerAlaasnIleSerArgGlyLeu	644
Db	2092	CATGTTCAGAGGACACGGCGCATTTGCAGATGCTGGCGCTCCAGCACTCCACGGCG---	2148
OY	645	GlnPheIleLeuThrProAsnGlnPheSerAlaGlnThrPheTyrAlaLeuSerProThr	664
Db	2148	-----	2148
OY	665	MetHisSerGlnAlaThrGlnValProLieserGlnSerAspGlySerAlaValAlaAla	684
Db	2148	-----	2148


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QY 383 MetalaserProArgIyGlnSerIleLysSerArgGlnAlaSerValGlyAsp----- 400
    ::::::::::::::::::::
Db 1246 TTTCACGACCCCGCAGGCGATGGCTGCCAAGGAAGGGGTCTCCCGACGCCAGACGCTC 1305
QY 401 ArgArgSerProSerThrAspIleThrAlaGluLysSerProThrLysValGlnLysSer 420
    ::::::::::::::::::::
Db 1306 CGGGGGTCCCCCACTGGCGATCAGATCTTATGACACCCCGACAGCGATGGCCCAAGAC 1365
QY 421 TrpSerPheAsnAspArgThrArgPheArgProSerLeuArgLeuLysSerGlnPro 440
    ::::::::::::::::::::
Db 1366 TGGAGCTTTGGTGCACCCCGACGCCAGCAGCGCTTTCGCGATCAAGGGTCTCATCC 1425
QY 441 LysFroValIleAspAlaAspThrAlaLeuGlyThrAspAspValTyrAspGlnLysGly 460
    ::::::::::::::::::::
Db 1426 CGCGAGATTTCAGAACGACAGCTCCCT---GGGAGACACATCGTGAAGACAGACAGAC 1482
QY 461 CysGlnCysAspValSerValGluAspLeuThrProProLeuLysThrValIleArgAla 480
    ::::::::::::::::::::
Db 1483 TGTAACTGCGAGTTTGTACTGAAGATCTTACCCCTGCGCTCAAGATTAGCATCAGAGCT 1542
QY 481 IleArgIleMetLysPheHisValAlaLysArgLysPheLysGlnThrLeuArgProThr 500
    ::::::::::::::::::::
Db 1543 GTCTGTGTATCCGCTCTTGTATCTAAGCCAAAGTTCAAGAGAGTCTGGCCCATAT 1602
QY 501 AspValLysAspValIleGluGlnTyrSerAlaGlnHisLeuAspMetLeuGlyArgIle 520
    ::::::::::::::::::::
Db 1603 GATGTGATGACGATCGAATCGAAGACTACTCGGCTGGACACTTGGAATCTGTGCCGATC 1662
QY 521 LysSerLeuGlnThrArgValAspGlnIleLeuGlyLysGlnIleThrSerAspLys 540
    ::::::::::::::::::::
Db 1663 AAGAGCTGAGTCCAGACAGTGCACCAATGTGTGGCGGGGCCCAACAATACGAT--- 1719
QY 541 LysSerArgGlnLysIleThrAlaGlnHisGlnThrThrAspAspLeuSerMetLeuGly 560
    ::::::::::::::::::::
Db 1720 AAGGATCGCACCAGAGCCGACGGAAGAGAGCTGCCCGCAAGACCCAGCATGTGGCA 1779
QY 561 ArgValValLysValGlnLysGlnValGlnSerIleGlnSerLysLeuAspCysLeuLeu 580
    ::::::::::::::::::::
Db 1780 CGGCTGTGGAGGTGGAGAAACAGGCTTGTCCATGTGAAAGAACGTCGACTTCTGGTG 1839
QY 581 AspIleTyrGlnGlnValLeuArgLysGlySerAlaSerAlaLeuAlaLeuAlaSerPhe 600
    ::::::::::::::::::::
Db 1840 AGCATCTATACACAG---AGATATGGC----- 1863
QY 601 GlnIleProProPheGluCys-----GluGlnThrSer 611
    ::::::::::::::::::::
Db 1864 ---ATCCCAACACAGACAGACAGAGCCTATTTTGGGCGCAAGAGCCTGACCCGCCACCA 1920
QY 612 AspTyrGlnSerProValAspSerLysAspLeuSerGlySerAlaGlnAsnSerGlyCys 631
    ::::::::::::::::::::
Db 1921 CCTTACCACAGCCCAAGAGACACCCCGTGAC-----CATGCAGACAAACCATGGCTGT 1971
QY 632 ---LeuSerArgSerThrSerAlaAsnIleSerArgGlyLeuGlnPheIleLeu 648
    ::::::::::::::::::::
Db 1972 ATCATTAAGATCTCTCCGCTCCACACCTCT----- 2001
QY 649 ThrProAsnGlnPheSerAlaGlnThrPheTyrAlaLeuSerProThrMetHisSerGln 668
    ::::::::::::::::::::
Db 2002 ---ACGGCCAGAGAGAACTACGACACACCCCGAGCATC-----CCC 2040
QY 669 AlaThrGlnValProIleSerGlnSer 677
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Db 2041 CCTGCCAGTGTCTCTCCCTCCACCTCG 2067

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RESULT 9

```

US-10-128-870-26
: Sequence 26, Application US/10128870
: Patent No. US20020168724A1
: GENERAL INFORMATION:
: APPLICANT: Bliane, Michael A.
: APPLICANT: Dworetzky, Steven
: APPLICANT: Grikoff, Valentin K.
: APPLICANT: Levesque, Paul C.

```

```

: APPLICANT: Little, Wayne A.
: APPLICANT: Neubauer, Michael G.
: APPLICANT: Yang, Wen-Pan
: TITLE OF INVENTION: KNO POTASSIUM CHANNELS AND METHODS OF MODULATING SAME
: FILE REFERENCE: DC584DIY
: CURRENT APPLICATION NUMBER: US/10/128,870
: PRIOR FILING DATE: 2002-04-24
: PRIOR APPLICATION NUMBER: 09/105,058
: PRIOR FILING DATE: June 26, 1998
: PRIOR APPLICATION NUMBER: 60/055,599
: PRIOR FILING DATE: August 12, 1997
: NUMBER OF SEQ ID NOS: 28
: SOFTWARE: Patentl Ver. 2.1
: SEQ ID NO 26
: LENGTH: 2565
: TYPE: DNA
: ORGANISM: Homo sapiens
: US-10-128-870-26

Alignment Scores:
Pred. No.: 1,56-147 Length: 2565
Score: 1587.50 Matches: 386
Percent Similarity: 54.61% Conservative: 106
Best Local Similarity: 42.84% Mismatches: 244
Query Match: 34.91% Indels: 165
Gaps: 28

US-09-810-796-5 (1-888) x US-10-128-870-26 (1-2565)
QY 3 AspValGlnSerGlyArgValLeuLeuAsnSerAlaAlaArgGlyAspGly 22
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Db 91 GACGTGGAGCA-----GTCACCTTGGCGTGGGGCGGAGCGCAAGAGCGG 141
QY 23 LeuLeuLeuGlyThrArgAlaAlaThrLeuGlyGlyGlyGlyLeuArgGlu 42
    ::::::::::::::::::::
Db 142 ACCCTCTGCTG-----GAGGGCGGCGCGCGCGAGAGCGG 177
QY 43 SerArgGlyLysGlnGlyAlaArgMetSerLeuLeuGlyLys---ProLeuSerTyr 61
    ::::::::::::::::::::
Db 178 CAGCGAGAGACCCCGCAGAGGC-----ATCGGCTCTGGCCCAAGACCCGCTGAGCGC 231
QY 62 ThrSerSerGlnSerCysArgArgAsnValLysTyrArgArgValGlnAsnTyrLeuTyr 81
    ::::::::::::::::::::
Db 232 CCAGTCAAG-----AGAAACAAGCCCAAGTACCGGGGCAATCCAACTTGTATCTAC 282
QY 82 AsnValLeuGlnArgProArgIleTyrPalaPheIleTyrHisAlaPheValPheLeuLeu 101
    ::::::::::::::::::::
Db 283 GACGCCCTGGAGACCGCGGGGCTGGCGCTGCTTACCAACGCGTGTGTTCTGATT 342
QY 102 ValPheGlyCysLeuIleLeuSerValPheSerThrIleProGlnHisThrLysLeuAla 121
    ::::::::::::::::::::
Db 343 GTTCCTGGGGTCTTGTATCTTGTGCTGTCTGACCAATTCAGAGAGTGGAGACTGTCTCG 402
QY 122 SerSerCysLeuLeuIleLeuGlnPheValMetIleValValPheGlyLeuGluPheIle 141
    ::::::::::::::::::::
Db 403 GGAGACTGGCTCTCTTACTGAGACATTTGATTTTCACTTTGGAGCGCAATTTGCT 462
QY 142 IleArgIleTrpSerAlaGlyCysCysArgTyrArgGlyTyrPalaArgLeuArg 161
    ::::::::::::::::::::
Db 463 TTGAGGATCTGGCGTGGCTGATGTTCTGCGCATACAAAGGTGGCGGGCCGACACTGAG 522
QY 162 PheAlaArgLysProPheGlyValIleAspThrIleValLeuLeuAlaSerIleAlaVal 181
    ::::::::::::::::::::
Db 523 TTTCGAGGAAGCCCTCTGTCATGTGGACATCTTTGTGCTGATGCTGTGCCAGTG 582
QY 182 ValSerAlaLysThrGlnLysAsnIlePheAlaThrSerAlaLeuArgSerLeuArgPhe 201
    ::::::::::::::::::::
Db 583 GTTGTGTGGAAACCAAGCAATTTCTGGCCACCTCC---CTGGGAACCTGGCGCTTC 639
QY 202 LeuGlnIleLeuArgMetValArgMetAspArgArgGlyGlyThrTrpLysLeuLeuGly 221
    ::::::::::::::::::::
Db 640 CTGCAATCTCGCATGCTCGGATGGACCGAGAGGTGGGCACTGGAAGCTTCTGGGC 699

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QY 222 SerValValYrAlaHisSerLysGluLeuIlePheAlaIlePheTyrIleGlyPheLeuVal 241
DB 700 TCACCCATCTGTCGCCACAGCAAGAACTCATACAGGCTGGTATAGTGTTCCTGACA 759
QY 242 LeuIlePheSerPheLeuValTyrLeuValGluLysAspAla----- 256
DB 760 CTCATCTCTTCTTCTTCTTCTGCTACTGCTGTGAGAAAGACCTCCAGAGGTGATGCA 819
QY 257 -----AsnLysGluPheSerThrTyrAlaAspAlaLeuTyrIlePheGlyThr 271
DB 820 CAAGAGAGAGAGATGAAGAGAGATTTGAGACCTATGACAGATGCCCTTGCGGGGCTG 879
QY 272 IleThrLeuThrThrIleGlyTyrGlyLysPheThrProLeuThrTyrLeuGlyArgLeu 291
DB 880 ATCACACTGGCCCATTTGGCTATGAGACAGACACCAACCGGGAGAGCGCTGTG 939
QY 292 LeuSerAlaGlyPheAlaLeuLeuGlyLysSerPhePheAlaLeuProAlaGlyIleLeu 311
DB 940 ATTCCCGCACCTTTCTCTTATTTGGCTCTCTTTTGGCTTCCCTCCAGCGGCGATCTG 999
QY 312 GlySerGlyPheAlaLeuLysValIleGluIleHisArgGlnLysHisPheGlyLysArg 331
DB 1000 GGGTCGGGCTGCGCCCTCAAGGTGACAGGACCAACCGTCAGAGACACTTTGAGAAAG 1059
QY 332 ArgAsnProAlaAlaAsnLeuIleGlnCysValTyrPargSerTyrAlaAlaAspGlyLys 351
DB 1060 AGGAAGCCAGCTGCTGAGCTTCACTTCAGGCTGCGTGGAGGTATTATCTCAACACCCCAAC 1119
QY 352 SerValSer-----IleAlaThrTyrLys-----ProHisLeu 362
DB 1120 AGGATTGACGCTGGTGGCAGACATGAGATTTTATGATGACGTGCTCTTCTTCTTCTTC 1179
QY 363 LysAlaLeuHisThrCysSerProThrAsnGlnLysLeuSerPheLysGluArgValArg 382
DB 1180 AGGAAGAACAAGCTGGAGGACGATCCAGCCAAAGCTGGCTCTTGGATCGGTTGCG 1239
QY 383 MetIleSerProArgGlyGlnSerIleLysSerArgGlnAlaSerValGlyAspArgArg 402
DB 1240 CTTCCTATCTCTGTTGTAACATACTA-----GGAAGCTATTT 1281
QY 403 SerProSerThrAspIleThrAlaGluGlySerProThrLysValGlnLysSerTyrPser 422
DB 1282 ACCCTTCGATGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1341
QY 423 PheAsnAspArgThrArgPheArgProSerLeuArgLeuLys----- 436
DB 1342 TTAAACATTAAGAGCGTTTCGACAGCGCTTCGATGAAAGCCCTACGCTTCTGCGAC 1401
QY 437 SerSerGlnProLysProValIleAspAlaAspThrAlaLeuGlyThrAspAspValTyr 456
DB 1402 AGTTCTGAA-----GATGCGGGACAGGT-----GACCCCATGGCG 1437
QY 457 AspGluLysGlyCysGlnCysAspValSerValGluAspLeuThrProProLeuLysThr 476
DB 1438 GAAGACAGGGGCTATGAGATGATCTCCCATGAGACATGATGATGATGATGATGATGATGATGAT 1497
QY 477 ValIleArgAlaIleArgIleMetLysPheHisValAlaLysArgLysPheLysGluThr 496
DB 1498 GCCATCCGAGCGCTGAGATTTCTACATTCGCTCTATTAATAAATAAATTCAGAGGACT 1557
QY 497 LeuArgProTyrAspValLysAspValIleGluGlnTyrSerAlaGlyHisLeuAspMet 516
DB 1558 TTGAGGCTTACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1617
QY 517 LeuCysArgIleLysSerLeuGlnThrArgValAspGlnIleLeuGlyLysGlyGlnIle 536
DB 1618 CTTTCAGAGATTAAGACTCTTCAGACGAGATATGATGATGATGATGATGATGATGATGATGAT 1677
QY 537 ThrSerAspLysLysSerArg----- 543
DB 1678 TCCACGCCAACAACACAGAAAGTCTCGAAAGGCTGACATTCACCTTCCATCCACAGCA 1737
QY 544 -----GluLysIleThrAlaGlnHisGluThr-----AspAspLeuSer 557

DB 1738 TCCTCCAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1797
QY 558 MetLeuGlyArgValValLysValGluLysGlnValGlnSerIleGluSerLysLeuAsp 577
DB 1798 ATGATGGGAGAGTTTGTAAAGTTGAAAGACAGGTTCAGACATGGGAGAGAGCTGAGC 1857
QY 578 CysLeuLeuAspIleTyrGlnGlnValLeuArg----- 588
DB 1858 TTCCTGCTGATATGACATGACATGACATGACATGACATGACATGACATGACATGACATGAT 1917
QY 589 -----LysGlySerAlaSerAlaLeuAlaLeuAlaSerPheGlnIleProPhe 605
DB 1918 TACCCACCAAGGCGACCTCTCTG-----CCAGCT 1947
QY 606 GluGlyGlnGlnThrSerAspTyrGlnSerProValAspSerLysAspLeuSerGlySer 625
DB 1948 GAAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2004
QY 626 AlaGlnAsnSerGlyCysLeuSerArgSerThrSerAlaAsnIleSerArgGlyLeuGln 645
DB 2005 TATTCTAGACAGGCGCCCGGACACACCTTACAGCTTCCAC----- 2046
QY 646 PheIleLeuThrProAsnGluPheSerAlaGlnThrPheTyrAlaLeuSerProThrMet 665
DB 2047 ---CAGTGACCAATTAAGCAAGATCAGCCCTATGGGTTTTCGACATGACCT----- 2097
QY 666 HisSerGlnAlaThrGlnValProIleSerIleSerAspGlySerAlaValAlaAlaThr 685
DB 2098 -----GTAAACCTGCCCCGAGGGGACCCAGTCTGGAAGGTTCAAGGCACT 2145
QY 686 AsnThrIleAlaAsnGlnIleAsnThrAlaProLysProAlaAlaProThrThrLeuGln 705
DB 2146 -----CTCTCTTCTGACGACACAGATGTTGGAG 2175
QY 706 IleProProProLeuProAlaIleLysHisLeuProArgProGluThrLeuHisProAsn 725
DB 2176 AGGCCACAGGCTGCTGCTATCTGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2232
QY 726 ProAlaGlyLeuGlnGlnSerIleSerAspValThrThrCysLeuValAlaSerLysGlu 745
DB 2233 CAGCTGACCTGACAGGCGCCCTACTGCGAC----- 2262
QY 746 AsnValGlnValAlaGlnSerAsnLeuThrLysAspArgSerMetArgLysSerPheAsp 765
DB 2263 CGAATTCGCCCGGCGAC-----AGAGCTGACATCAGC 2295
QY 766 MetGlyGlyGlnThrLeuLeuSerValCysProMetValProLysAspLeuGlyLysSer 785
DB 2296 CGAAGACAGTGCACACACCTGCTCCCTG----- 2322
QY 786 LeuSerValGlnAsnLeuIleArgSerThrGlnGluLeuAsnIleGlnLeuSerGlySer 805
DB 2323 ATGTGCGTCAACAC-----GAGGAGCTGGAGAGGTCTCCAAAGTGAGCTTC 2367
QY 806 GluSerSerGlySerArgLysSerGlnAspPheTyrPro-----LysTyrArg 821
DB 2368 AGCATCTCCAGACAGAGAGATATATGTTGCGCCCAATGGGGGTCGAGCGATG 2427
QY 822 GluSerLysLeuPheIleThrAspGluGluValGlyProGluGlnThrGluThrAspThr 841
DB 2428 AGGAGAGAGCGGTACCTGCGCAG-----GCTGAGACGACACAGACAGGAGCC 2478
QY 842 Phe 842
DB 2479 TTC 2481

RESULT 10
US-10-128-870-5
; Sequence 5, Application US/10128870
; Patent No. US20020168724A1
; GENERAL INFORMATION:
; APPLICANT: Blandar, Michael A.

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; APPLICANT: Dworetzky, Steven
; APPLICANT: Gribkoff, Valentin K.
; APPLICANT: Levesque, Paul C.
; APPLICANT: Little, Wayne A.
; APPLICANT: Neubauer, Michael G.
; APPLICANT: Yang, Wen-Pin
; TITLE OF INVENTION: KCNO POTASSIUM CHANNELS AND METHODS OF MODULATING SAME
; FILE REFERENCE: DC58adiV
; CURRENT APPLICATION NUMBER: US/10/128,870
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 09/105,058
; PRIOR FILING DATE: June 26, 1998
; PRIOR APPLICATION NUMBER: 60/055,599
; PRIOR FILING DATE: August 12, 1997
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 900
; TYPE: DNA
; ORGANISM: MOUSE
; FEATURE:
; OTHER INFORMATION: 900 nucleotides of murine KCNQ2
US-10-128-870-5

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Alignment Scores:
Pred. No.: 1,41e-110 Length: 900
Score: 1207.50 Matches: 227
Percent Similarity: 83.88% Conservative: 28
Best Local Similarity: 74.67% Mismatches: 40
Query Match: 26.56% Indels: 9
DB: Gaps: 2

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US-09-810-796-5 (1-888) x US-10-128-870-5 (1-900)

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QY 56 GlyylsProleuSerTyrThrSerSerGlnSerCysArGArGAsnValLysTyrArgArg 75
DB 13 GGGAAAGCCC-----CCGAAGCGCAAGCCCTTACCGCGAAG 48
QY 76 ValGlnAsnTyrLeuTyrAsnValLeuGlnArGProArGlyTyrPalapheleTyrHis 95
DB 49 CTGCAAGATTCTCTACACAGCTGTAGAGCGGCCCGCGGCGGCTTCATCTACAC 108
QY 96 AlaPheValPheLeuLeuValPheGlyCysLeuLeuLeuSerValPheSerThrIlePro 115
DB 109 GCCTACGTTCTCTTAGTCTTCTCCCTGCTTGTCTTCTGTTTCACACATCAAG 168
QY 116 GluHisThrLysLeuAlaSerSerCysLeuLeuLeuGluPheValMetIleValVal 135
DB 169 GAGTACGAGAAAGAGCTGTAGAGGGGCCCTTACATCTTGGAATGTGATCTGTGTA 228
QY 136 PheGlyLeuGluPheIleIleIleArgIleTyrSerAlaGlyCysCysArgTyrArgly 155
DB 229 TTGGGCTGTAGTACTTGTGGAGATCTGGGCTGAGGCTCTGTTGCCGATACGAGGC 288
QY 156 TrpGlnGlyArgLeuArgPheAlaArgLysProPheCysValIleAspThrIleValLeu 175
DB 289 TGGAGGGCGAGCGCTCAAGTTTCCAGAGAGCGCTTGTGTGATGATGATGATGATG 348
QY 176 IleAlaSerIleAlaValAlaSerAlaThrGlnGlnLysIlePheAlaThrSerAla 195
DB 349 ATTGCTCCATTTCTGCTGCGGCTGCTCCAGGAGGATGCTTGGCCACATCTCGC 408
QY 196 LeuArgSerLeuArgPheLeuGlnIleLeuAlaArgMetValaArgMetAspArgArgly 215
DB 409 CTTCGAGCGTTGGGCTTCTTGCACAAATCTTGGGATGATCCGTAAGGAGCGGCTG 468
QY 216 ThrTrpLysLeuLeuGlnLysValValTyrAlaHisSerLysGluLeuIleThrAlaTrp 235
DB 469 ACCGTGAAGCTCTTGGGATCGTAGCTACGCTACAGCAAGAGCGTGTACCTGCG 528
QY 236 TyrIleGlyPheLeuValLeuIlePheSerSerPheLeuValTyrLeuValGluLysAsp 255
DB 529 TACATTGGCTTCTCTGCTCATCTGAGGCTCATTTCTGTGTAATTGAGCAAAAGGT 588

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QY 256 AlaAsnLysGluPheSerThrTyrAlaAspAlaLeuTrpTrpGlyThrIleThrLeuThr 275
DB 589 GAGATGACCACTTTTACACACTTACGACAGATGACACTGTGGGGCTGTGATCACCCTGACG 648
QY 276 ThrIleGlyTyrGlyLysPheThrProLeuThrTrpLeuGlyArgLeuSerAlaGly 295
DB 649 ACCATTGGCTACGGGAGCAAGTACCTCAGACCTGGAGCGGAGGCTGTGGCAGCACC 708
QY 296 PheAlaLeuGlyLysSerPhePheAlaLeuProAlaGlyIleLeuGlySerGlyPhe 315
DB 709 TTTACCTATTGGTGTCTGCTTCTTCTTCTGCTGCTGCGCATTTTGGCATTCGGCTT 768
QY 316 AlaLeuLysValGlnGlnIleHisArgGlnLysHisPheGlyLysArgArgAsnProAla 335
DB 769 GCCGTGAAGTCCAGAGAGCAGCATCGGCAAAACACTTTGAGAAAGCGGAGAACCTGCG 828
QY 336 AlaAsnLeuIleGlnCysValTyrPArgSerTyrAlaAlaAspLysSerValSerIle 355
DB 829 GCAGGTGTGATCAGCTGCTGCTGAGATTTCTAGTAACCTTCACGACCGACCTG 888
QY 356 --AlaThrTrp 358
DB 889 CACTCCACTGTG 900

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RESULT 11
US-10-128-870-3
; Sequence 3, Application US/10128870
; Patent No. US20020168724A1
; GENERAL INFORMATION:
; APPLICANT: Blau, Michael A.
; APPLICANT: Dworetzky, Steven
; APPLICANT: Gribkoff, Valentin K.
; APPLICANT: Levesque, Paul C.
; APPLICANT: Little, Wayne A.
; APPLICANT: Neubauer, Michael G.
; APPLICANT: Yang, Wen-Pin
; TITLE OF INVENTION: KCNO POTASSIUM CHANNELS AND METHODS OF MODULATING SAME
; FILE REFERENCE: DC58adiV
; CURRENT APPLICATION NUMBER: US/10/128,870
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 09/105,058
; PRIOR FILING DATE: June 26, 1998
; PRIOR APPLICATION NUMBER: 60/055,599
; PRIOR FILING DATE: August 12, 1997
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 900
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: 900 nucleotides of human KCNQ2
US-10-128-870-3

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Alignment Scores:
Pred. No.: 5,57e-110 Length: 900
Score: 1201.50 Matches: 226
Percent Similarity: 83.55% Conservative: 28
Best Local Similarity: 74.34% Mismatches: 41
Query Match: 26.42% Indels: 9
DB: Gaps: 2

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US-09-810-796-5 (1-888) x US-10-128-870-3 (1-900)
QY 56 GlyylsProleuSerTyrThrSerSerGlnSerCysArGArGAsnValLysTyrArgArg 75
DB 13 GGGAAAGCCC-----CCGAAGCGCAAGCGCTTACCGCGAAG 48
QY 76 ValGlnAsnTyrLeuTyrAsnValLeuGlnArGProArGlyTyrPalapheleTyrHis 95
DB 49 CTGCAAGATTCTCTACACAGCTGTGAGGCGGCCGCGGCGGCTTCATCTACAC 108

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QY 96 AlaPheValPheLeuValPheGlyCysLeuIleLeuSerValPheSerThrIlePro 115
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 109 GCTACGTTGCTCCCTGCTGTTTCTCCGCTCGCTGCTGCTGTTTCCACCAACG 168
QY 116 GluHisThrIleValSerCysLeuLeuIleGluPheValMetIleValVal 135
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 169 GAGTATAGAAAGACGTCGAGGCGGCTTACATCTGGAATGCTGATCTGCTG 228
QY 136 PheGlyLeuGluPheIleIleArgIleThrSerIleGlyCysCysArgThrArgGly 155
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 229 TTTCGCGGAGTACTCTGCTGCGGATCTGGGCGCAGGCTGCTGCTGCTGCTG 288
QY 156 TrpGlnGlyArgLeuArgPheAlaArgLysProPheCysValIleAspThrIleValLeu 175
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 289 TGGAGGGGGCGCTCAACTTTGGCCGGAACCGCTGCTGATTCATCATGCTGCTC 348
QY 176 IleAlaSerIleAlaValSerAlaLysThrGlnGlyAsnIlePheIleThrSerAla 195
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 349 ATCGCTCATTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 408
QY 196 LeuArgSerLeuArgPheLeuGlnIleLeuArgMetValArgMetAspArgArgGly 215
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 409 CTCGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 468
QY 216 ThrTrpLysLeuLeuGlySerValValIleAlaHisSerLysGluLeuIleThrAlaTrp 235
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 469 ACCGTGAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 528
QY 236 TyrIleGlyPheLeuValLeuIlePheSerSerPheLeuValIleValLysAsp 255
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 529 TACATCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 588
QY 256 AlaAsnLysGluPheSerThrTrpAlaAspAlaLeuTrpTrpGlyThrIleThrLeuThr 275
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 589 GAGAAGACGACCTTGAACACCTACCGGATGACCTGCTGCTGCTGCTGCTGCTG 648
QY 276 ThrIleGlyTyrGlyAspLysThrProLeuThrTrpLeuGlyArgLeuSerAlaGly 295
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 649 ACCATTGGCTACGAGGAGCAAGTACCCAGACCTGGAAGGAGGCTCTTGGCGCAAC 708
QY 296 PheAlaLeuLeuGlyLysSerPhePheAlaLeuProAlaGlyIleLeuGlySerGlyPhe 315
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 709 TTCACCTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 768
QY 316 AlaLeuLysValGlnGlnIleHisArgGlnLysHisPheGluLysArgArgAspProAla 335
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 769 GCCCTGAAGGTCAGGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 828
QY 336 AlaAsnLeuIleGlnCysValIleTrpArgSerTrpAlaAlaAspGluLysSerValSerIle 355
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 829 GCAGGCTGATCCAGTGGGCTGAGATTTTACCCACCAACCTCTGCCGACAGACCTG 888
QY 356 ---AlaThrTrp 358
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 889 CACTCCACGCTGG 900

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RESULT 12
US-09-840-125-1
Sequence 1, Application US/09840125
Patent No. US20020061524A1

GENERAL INFORMATION:
APPLICANT: Splawski, Igor
TITLE OF INVENTION: ALTERATIONS IN THE LONG QT SYNDROME GENES KVLQT1 AND
FILE REFERENCE: 2323-155
CURRENT APPLICATION NUMBER: US/09/840.125
PRIOR FILING DATE: 2001-04-24
PRIOR APPLICATION NUMBER: 09/634,920
PRIOR FILING DATE: 2000-08-09
PRIOR APPLICATION NUMBER: 60/147,488
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 4

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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 2028
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2028)
; US-09-840-125-1

Alignment Scores:
Pred. No.: 1.01e-100 Length: 2028
Score: 1114.00 Matches: 268
Percent Similarity: 55.29% Conserved: 108
Best Local Similarity: 39.41% Mismatches: 199
Query Match: 24.50% Indels: 105
DB: Gaps: 18

US-09-810-796-5 (1-888) x US-09-840-125-1 (1-2028)

QY 7 GlyArgGlyArgValLeu---LeuAsnSerAlaAlaAlaArgGlyAspGlyLeuLeu 25
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 27 GCGCAGAGAGAGAGCGCTGGGTTGGGGCCCGCTGCCAGCGCGCGGGGCGAGCGGG 86
QY 26 LeuGlyThrArgAlaAlaThrLeuGlyGlyGlyGlyGlyGlyLeuArgLysSerArgArg 45
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 87 CCTGGCAGAAAGTCCCTCTGCTGAGCTGGCGGAGGCGGCGCGCGCGCGCGCGCG 146
QY 46 GlyLysGlnGlyAlaArgMet----- 52
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 147 GCTATACGCGCCATGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 206
QY 53 -----SerLeuLeuGlyLysProLeu-Se 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 207 GCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 266
QY 60 rTyThrSerSerGlnSerCysArgArgAsnValLysTyArg---ArgValGlnAsnTy 79
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 267 GCGCGCTTCATCTACAGCAGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 326
QY 79 rLeuTyArgAsnValLeuGlnArgProArgGlyLys---AlaPheIleThrHisAlaPheVal 98
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 327 CGCTACACACTTCTCTGAGCGTCCACCGCGCTGGAATGCTGTATACCATCTCGCGCT 386
QY 98 lPheLeuLeuValPheGlyCysLeuIleLeuSerValPheSerThrIleProGlnHisThr 118
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 387 CTTCCTCATCGTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 446
QY 118 rLysLeuAlaSerSerCysLeuLeuIleLeuGluPheValMetIleValValPheGlyLe 138
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 447 CGCCCTGGCCAGCGGAGCTCTCTTCTGATGAGATGCTGCTGCTGCTGCTGCTGCTG 506
QY 138 uGluPheIleIleArgIleThrSerAlaGlyCysCysArgTyArgGlyTrpGlnGly 158
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 507 GAGTACGTCGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 566
QY 158 yArgLeuArgPheAlaArgLysProPheCysValIleAspThrIleValLeuIleAlaSe 178
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 567 GCGGCTGCGCTTGGCCCGGAGGCCATTTCCATCATGACCTCATCTGCTGCTGCTGCTG 626
QY 178 rIleAlaValValSerAlaLysThrGlnGlyAsnIlePheAlaThrSerAlaLeuArgSe 198
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 627 CATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 686
QY 198 rLeuArgPheLeuGlnIleLeuArgMetValArgMetAspArgArgGlyTrpTrpLys 218
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 687 CATCCGCTTCTGAGATCTGAGATGCTACACCTGACCGCCAGGAGGACCTTGAG 746
QY 218 sLeuLeuGlySerValValIleAlaHisSerLysGluLeuIleThrAlaTrpTyIleGly 238
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 747 GCTCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 806
QY 238 yPheLeuValLeuIlePheSerSerPheLeuValIleValValGluLysAspAla----- 256

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Db 481 ATCAGGGGATCCCTTCTCTGAGATCTGAGATGTCACGTCGACCGCCAGGAGGAGC 540
 Oy 216 ThrThrPheLeuLeuGlySerValValThrAlaHisSerLysGluLeuLeuThrAlaTrp 235
 Db 541 ACCGGAAGGCTCCGGGCTCCGCTTTCATCCACCCGCGAGAGCTGATTAACCCACCTCG 600
 Oy 236 TyrTLeuGlyPheLeuValLeuLeuPheSerSerPheLeuValTyrLeuValGluLysAsp 255
 Db 601 TACATCGGCTTCTGGGCTCATCTTCTCTCTGATCTTGTGTACTGGCTGAGAGGAGC 660
 Oy 256 Ala-----AsnLysGluPheSerThrTyrAlaAspAlaLeuTrpPgly 270
 Db 661 GCGGAGACGAGTCAGCGCGCGCTGAGATTCCGCGACGACGACATCCGCTGTGTGGGG 720
 Oy 271 ThrLeuThrLeuThrThrLeuGlyTyrGlyAspLysThrProLeuThrThrLeuGlyArg 290
 Db 721 GTGGACACAGTCACACCATCGGCTATGGGACAGAGTGGCCCGACAGCGTGGGAGAG 780
 Oy 291 LeuLeuSerAlaGlyPheAlaLeuLeuGlyLysSerPhePheAlaLeuProAlaGlyTle 310
 Db 781 ACCATCGGCTCTGCTCTCTCTGCTTGGCATCTCTCTTCTTGGCTCCGACGGGGATT 840
 Oy 311 LeuGlySerGlyPheAlaLeuLysValGlnGlnGlnHisArgGlnLysHisPheGluLys 330
 Db 841 CTGGGCTGGGGCTTGGCTGAGGTCAGACAGACAGACAGACAGACAGACAGACAGACAG 900
 Oy 331 ArgAlaGlnProAlaAlaAsnLeuLeuGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 350
 Db 901 CAGATCCCGCGGCGAGCTCTACTCTATTCAGACCGCATGGAGGTGCTATGCTGCCGAGAC 960
 Oy 351 LysSerValSerTleAlaThrThrLysProHisLeuLysAlaLeu-----HisThr 367
 Db 961 CCCGACTCTCC-----ACCTGGAAGATCTACATCCGAGAGCGCCCGGAGCGACT 1014
 Oy 368 ---CysSerProThrAsnGlnLysLeuSerPheLysGluArgAlaMetAlaSerPro 386
 Db 1015 CTGCTCTACCCAGCCCAACCC-----AAGAAGTCTGTGGTGGTAAAGAAAAA 1065
 Oy 387 ArgGlyGlnSerTleLysSerArgGlnAlaSerValGlyAspArgLysSerProSerThr 406
 Db 1066 AAGTTCAGCTGACAAAGAACAAATGGGGTACTCTGAGAGAGAGATGCTCAGATCCCC 1125
 Oy 407 AspTleThrAlaLeuGlySerProThrLysValGlnLysSerTrpSer-----Phe 423
 Db 1126 CATATCAGCTGCGACCCCGACAGAGAGCGGGCTGACACCATCTCTCTGAGACGGCAT 1185
 Oy 424 AsnAspArgThrArgPheArgProSerLeuArgLysSerSerGlnProLysProVal 443
 Db 1186 GACAGTTCCTGAAGGAGAGAGCCCAACTG---CTGGAAAGTGAAGCATGCCCAT 1236
 Oy 444 TleAspAlaAspThrAlaLeuGlyThrAspAspValTyrAlaArgLysGlyCysGlnCys 463
 Db 1237 -----TTCATGAGAACCAACAGCTTCCCGGAGGAC-----CTG 1269
 Oy 464 AspValSerValGluAspLeuThrProProLeu----- 474
 Db 1270 GACCTGGAAGGAGGACTCTCTGACACCCATACCCACATCTCAGCTGCGGGAACAC 1329
 Oy 475 ---LysThrValIleArgAlaIleArgIleMetLysPheHisValAlaLysArgLysPhe 493
 Db 1330 CATCGGCGCACCATTAAGGTATTCGACGACATCTTGTGGCCCAAGAAATTC 1389
 Oy 494 LysGluThrLeuArgProTyrAspValLysAspValIleGlnGlnTyrSerAlaGlnHis 513
 Db 1390 CAGCAAGCGCGAAGGCTTACGATGCGGAGACGTCATTGACACAGTACGCGAGGGCCAC 1449
 Oy 514 LeuAspMetLeuCysArgIleLysSerLeuGlnThrArgValAspGlnIleLeuGlyLys 533
 Db 1450 CTCACACCTCAGTGGCGCATCAAGAGCTGCAGAGAGGCTGACACAGTCACTTGGGAAG 1509
 Oy 534 GlyIle-----IleThrSerAspLysSerArgGluLysIleThrAlaGlnHisGlu 551
 Db 1510 CCTCCTACTGTTCATCTCGTCTCAGAAAAAGAGAGGATGCG----- 1551

Oy 552 ThrThrAspLeuSerMetLeuGlyArgValValLysValGluLysGlnValGlnSer 571
 Db 1552 -----GCGACGAACACAGTCAGCGCGCGCTGAAACGAGTAAAGACAAAGGTGACGAG 1605
 Oy 572 TleGluSerLysLeuAspCysLeuLeuAspTleTyrGlnGlnValLeuArgLysGlySer 591
 Db 1606 CTGACCAAGAGGTGGGACATCATCACCAGCATGCTTTCACAGCTGTCTCTGACACGCT 1665
 Oy 592 -AlaSerAlaLeuAlaLeuAlaSerPheGlnIleProProPheGluLysGlnGlnThrSe 611
 Db 1666 GCGACGACACCGCGGACAGCGCGCGCC-----CCCCAGAGAGGCGGGGCGGACATC 1716
 Oy 611 AspTyrGlnSerProValAspSer-----LysAspLeuSerGlySer-AlaGlnAsnSerG 630
 Db 1717 ACCCAGCGCTCGGACAGTGGGCGGCTCCGCTCGACCTGACCTTCTCTGCGCCAGCAACAC 1776
 Oy 630 LysLysLeuSerArgSerThrSer-----AlaAsnIleSerA 642
 Db 1777 CTGCCCCACCTACGACGACTGACCGTCCCAAGAGGCGCCCGCATGAGGGGTCTGAGGA 1836
 Oy 642 rgGlyLeuGlnPheTleuThrProAsnGlnPheSerAlaGlnThrPhe-----TyrA 660
 Db 1837 GGGGATGGGCTGGGGGATGGGCTGAGTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAG 1896
 Oy 660 LysLeuSerProThrMetHis-----SerGlnAlaThrGlnValProLysSerGlns 677
 Db 1897 CCTCTCTGAAAGAGGACCATCTCTTAAAGGCCAGAGAGAGAGGAGGAGGAGGAGGAG 1955
 Oy 677 erAspGlySerAlaValAlaAlaThrAsnThrTleAlaAsnGlnIleAsnThrAlaProL 697
 Db 1956 -----GCCCCAA 1962
 Oy 697 ysProAlaAlaProThrThrLeuGlnIlePro-----ProProL 710
 Db 1963 TACCCGATGAGACATGCTGTCTGACACAGCTGCACTTGGGGGCTCAGCAAGGCCACCTG 2022
 Oy 710 euPro 711
 Db 2023 TTCCT 2027
 RESULT 14
 US-10-128-870-17
 ; Sequence 17, Application US/10128870
 ; Patent No. US20020168724A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Blauert, Michael A.
 ; APPLICANT: Dworetzky, Steven
 ; APPLICANT: Grikhoff, Valentin K.
 ; APPLICANT: Levesque, Paul C.
 ; APPLICANT: Little, Wayne A.
 ; APPLICANT: Neubauner, Michael G.
 ; APPLICANT: Yang, Wen-Pin
 ; TITLE OF INVENTION: KCNO POTASSIUM CHANNELS AND METHODS OF MODULATING SAME
 ; FILE REFERENCE: DC58adiy
 ; CURRENT APPLICATION NUMBER: US/10/128,870
 ; PRIOR FILING DATE: 2002-04-24
 ; PRIOR APPLICATION NUMBER: 09/105,058
 ; PRIOR FILING DATE: June 26, 1998
 ; PRIOR APPLICATION NUMBER: 60/055,599
 ; PRIOR FILING DATE: August 12, 1997
 ; NUMBER OF SEQ ID NOS: 28
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 17
 ; LENGTH: 930
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; OTHER INFORMATION: 930 nucleotides of human KCNQ3
 US-10-128-870-17
 Alignment Scores: 2.15e-98 Length: 930
 Pred. No.:

